

GenCore version 5.1.4-p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 04:39:54 ; Search time 171.5 seconds
(without alignments)
302.017 Million cell updates/sec

Title: US-09-975-842-2

Sequence: 1 gnnhlnccngntlymgnrtngg 23

Scoring table: IDENTITY_NUC

Gapop:10.0 , Gapext:1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N.Ceneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
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19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
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21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.4	67.3	23	9	AAV30328
2	15.4	67.3	23	24	AAV30328
3	15.4	67.3	748	24	ABO65439
4	15.4	67.3	961	19	AAV00220
5	15.4	67.3	968	17	AAV00219
6	15.4	67.3	993	17	AAV33139
7	15.4	67.3	1080	18	AAV72628
8	15.4	67.3	1096	18	AAV72631
9	15.4	67.3	1098	18	AAV72630

10	15.4	67.0	1104	18	AAV72629
11	15.4	67.0	1113	18	AAV72632
12	15.4	67.0	1170	18	AAV6247
13	15.4	67.0	1384	17	AAV33136
14	15.4	67.0	1482	13	AAQ25896
15	15.4	67.0	1703	12	AAQ15131
16	15.4	67.0	1703	12	AAQ15131
17	15.4	67.0	1703	12	AAV15701
18	15.4	67.0	1703	12	AAV15701
19	15.4	67.0	1775	22	AAV23618
20	15.4	67.0	1780	12	AAQ15138
21	15.4	67.0	1781	12	AAQ15137
22	15.4	67.0	1793	12	AAQ15136
23	15.4	67.0	1793	12	AAQ15136
24	15.4	67.0	1800	19	AAV09713
25	15.4	67.0	1818	12	AAQ15135
26	15.4	67.0	1818	22	AAQ4546
27	15.4	67.0	1828	23	ABLO9571
28	15.4	67.0	1868	18	AAV33502
29	15.4	67.0	1878	19	AAV30326
30	15.4	67.0	1888	19	AAV31482
31	15.4	67.0	1923	21	AAV2947
32	15.4	67.0	2088	19	AAV15704
33	15.4	67.0	2230	19	AAV15704
34	15.4	67.0	2230	22	AAQ4544
35	15.4	67.0	2230	22	AAQ23821
36	15.4	67.0	2438	20	AAV35671
37	15.4	67.0	2613	15	AAQ35241
38	15.4	67.0	2613	15	AAQ35241
39	15.4	67.0	2724	12	AAQ15140
40	15.4	67.0	7244	19	AAV15705
41	15.4	67.0	7244	22	AAQ4545
42	15.4	67.0	7244	22	AAV23622
43	15.4	67.0	7587	12	AAQ15133
44	15.4	67.0	7587	19	AAV15703
45	15.4	67.0	7587	22	AAQ4543

ALIGNMENTS

RESULT 1	AAV30328	standard; DNA; 23 BP.
ID	AAV30328	
XX	AAV30328:	
AC	28-SEP-1998	(first entry)
XX		
DF		
XX	ACC synthase gene PCR primer I.	
DB		
XX		
KW	ACC synthase; 1-aminocyclopropane-1-carboxylate synthase;	
KW	ethylene; transgenic plant; wilting; geranium; rose; PCR; primer;	
KW	ss.	
XX		
OS	Synthetic.	
OS	Pelargonium x hortorum.	
OS	Rosa sp.	
XX		
Key	Location/Qualifiers	
FT	modified_base	3
FT	modified_base	/*tag= a
FT	modified_base	/mod_base= i
FT	modified_base	6
FT	modified_base	/*tag= b
FT	modified_base	/mod_base= i
FT	modified_base	9
FT	modified_base	/*tag= c
FT	modified_base	/mod_base= i
FT	modified_base	12
FT	modified_base	/*tag= d
FT	modified_base	/mod_base= i
FT	modified_base	18

Carica papaya ACC
Mangifera indica A
ACC synthase GAC-2
Broccoli ACC synth
ACC synthetase gen
Clone pACC1 encod
Zucchini ACC synth
Zucchini 1-aminoc
Zucchini ACC synth
Clone pACC1 encod
Clone pACC4 encod
Clone pACC3 encod
Clone pACC6 encod
ACC synthase DNA.
Clone pACC2 encod
Tomato 1-aminocycl
Drosophila melanog
Poplar 1-aminocycl
Pelargonium 1-amin
Papaya ACC synthas
Mung bean ACC synt
Coffee fruit speci
Tomato ACC synthas
Tomato 1-aminocycl
Tomato ACC synthas
DNA encoding a 1-a
Crucifer 1-aminoc
Drosophila melanog
Genomic clone LE-A
Tomato ACC synthas
Tomato 1-aminocycl
Tomato ACC synthas
Zucchini ACC synth
Zucchini ACC synth
Zucchini CP-ACC 1B

```

FT      /*lag= e
FT      /mod_base= i
FT      21
FT      modified_base
FT      /mod_base= i
XX
XX      W09814465-A1.
XX
XX      09-APR-1998.
XX
XX      30-SEP-1997; 97WO-US17644.
XX
XX      01-OCT-1996; 96US-0724194.
XX
XX      (COLS ) UNIV COLORADO STATE RES FOUND.
XX
XX      Ranu RS;
XX
XX      WPI: 1998-260994/23.
XX
XX      New isolated ACC synthase genes - are obtained from geranium and
XX      rose, used to develop products for producing plants with reduced
XX      ethylene levels, for increasing shelf-life
XX
XX      Example; Page 36; 77pp; English.
XX
XX      Primer I and primer II (see AAV30329) were used in PCR amplifications
XX      to develop PCR probes for the isolation of geranium and rose
XX      1-aminocyclopropane-1-carboxylate synthase (ACC synthase) cDNA
XX      clones (see AAV30324-26 and AAV30330). The invention relates to the
XX      use of antisense fragments of these genes to control ACC synthase
XX      expression in plants. By reducing the amount of ACC synthase
XX      produced in plant cells, the rate of ACC conversion to ethylene
XX      can be decreased. This can be used to prolong the shelf-life of
XX      cut flowers and to reduce leaf yellowing and petal abscission
XX      during shipping and storage.
XX
XX      Sequence 23 BP; 0 A; 2 C; 7 G; 4 T; 10 other;
XX
XX      Query Match 67.0%; Score 15.4; DB 19; Length 23;
XX      Best Local Similarity 100.0%; Pred. No. 1.1e+02;
XX      Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      1 GGNYNCCGNGNTTYMGNTNGG 23
XX      ||||||||||||||||||||
XX      1 GGNYNCCGNGNTTYMGNTNGG 23
XX
XX      RESULT 2
XX      AAS19698
XX      ID AAS19698 standard: DNA; 23 BP.
XX
XX      AAS19698;
XX
XX      09-APR-2002 (first entry)
XX
XX      PCR primer #1 used to amplify DNA fragment of geranium pHSacc genes.
XX
XX      Geranium; 1-aminocyclopropane-1-carboxylate synthase gene promoter;
XX      ACC synthase; plant transcription regulation; plant; PCR primer;
XX      gPHSacc49; ss.
XX
XX      Pelargonium x hortorum.
XX
XX      W0200185754-A1.
XX
XX      15-NOV-2001.
XX
XX      09-MAY-2001; 2001WO-US15023.
XX
XX      09-MAY-2000; 2000US-203021P.
XX      12-OCT-2000; 2000US-239782P.
XX

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```

PA      (COLS ) UNIV COLORADO STATE.
PA      (TAGA-) TAGANA GREENHOUSES INC.
XX
XX      Ranu RS;
XX
XX      WPI: 2002-075241/10.
XX
XX      New promoter from the 1-aminocyclopropane-1-carboxylate synthase gene
XX      of geranium, useful to regulate level of transcription of coding
XX      sequence in geranium and other plants
XX
XX      Claim 7; Fig 2; 38pp; English.
XX
XX      The present invention relates to the isolation of promoter DNA from
XX      geranium (Pelargonium x hortorum) genomic clone pHSacc49 (gPHSacc49).
XX      This promoter represents the ACC (1-aminocyclopropane-1-carboxylate)
XX      synthase gene promoter. The promoter is useful to regulate the
XX      transcription level of a coding sequence in geranium and other plants.
XX      The present sequence represents a PCR primer used to amplify a DNA
XX      fragment of geranium pHSacc genes.
XX
XX      Sequence 23 BP; 0 A; 2 C; 7 G; 4 T; 10 other;
XX
XX      Query Match 67.0%; Score 15.4; DB 24; Length 23;
XX      Best Local Similarity 100.0%; Pred. No. 1.1e+02;
XX      Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      1 GGNYNCCGNGNTTYMGNTNGG 23
XX      ||||||||||||||||||||
XX      1 GGNYNCCGNGNTTYMGNTNGG 23
XX
XX      RESULT 3
XX      AB065439/C
XX      ID AB065439 standard: DNA; 748 BP.
XX
XX      AB065439;
XX
XX      21-AUG-2002 (first entry)
XX
XX      Arabidopsis thaliana polynucleotide SEQ ID NO 16.
XX
XX      Arabidopsis thaliana; thale cress; plant; transgenic; GNO; disease;
XX      stress; metabolic pathway; biosynthetic pathway; nutrition; fungicide;
XX      insecticide; antibiotic; ds.
XX
XX      Arabidopsis thaliana.
XX
XX      US2002059663-A1.
XX
XX      16-MAY-2002.
XX
XX      26-JAN-2001; 2001US-0770149.
XX
XX      27-JAN-2000; 2000US-178506P.
XX
XX      (GORL/) GORLACH J.
XX      (ANY/) AN Y.
XX      (HAM/) HAMILTON C M.
XX      (PRIC/) PRICE J L.
XX      (RAIN/) RAINES T M.
XX      (YUY/) YU Y.
XX      (RAME/) RAMEKA J G.
XX      (PAGE/) PAGE A.
XX      (MATH/) MATHEW A V.
XX      (LEDF/) LEDFORD B L.
XX      (WORS/) WORESSNER J P.
XX      (HAAS/) HAAS W D.
XX      (GARC/) GARCIA C A.
XX      (KRIC/) KRICKER M.
XX      (SLAT/) SLATER T.
XX      (DAVI/) DAVIS K R.
XX      (ALLE/) ALLEN K.

```

PA (HOFF/) HOFFMAN N.
 XX (HURB/) HURBAN P.
 PI Goriach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y,
 PI Rameek JG, Price A, Mathew AV, Ledford BL, Woessner JP, Haas WD,
 PI Garcia CH, Kricker M, Slater T, Davis RK, Allen K, Hoffman N,
 PI Hurban P;
 DR WPI: 2002-47924/51.
 XX
 PT New nucleic acid that hybridizes to Arabidopsis thaliana sequences,
 PT useful e.g. for preparing transgenic plants with increased resistance
 PT or altered metabolism
 XX
 PS Claim 1: SEQ ID NO 16; 40bp + Sequence Listing: English.
 CC The invention relates to nucleic acids (I) that hybridise under stringent
 CC conditions to any of 999 sequences (AB065424-AB066422) or their
 CC fragments. (II) are used to suppress the corresponding polypeptides (II) or
 CC to produce genetically modified plant cells or transgenic plants, which
 CC may have improved resistance to disease stress, or altered
 CC metabolic/biosynthetic pathways (for production of commercial
 CC nutritional or medicinal products) or generally any trait of interest,
 CC or can be used to screen for biologically active agents (e.g. fungicides,
 CC insecticides and antibiotics) or generally any trait of interest.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from the
 CC USPTO at seqdata.uspto.gov/sequence.html?docid=9990970149.
 CC
 SO Sequence 748 BF; 209 A; 202 C; 120 G; 213 T; 4 other;
 Query Match
 Best Local Similarity 67.0%; Score 15.4; DB 24; Length 748;
 Matches 13; Conservative 56.5%; Pred. No. 1.5e+02; Indels 0; Gaps 0;
 Mismatches 6;
 OY 1 GGNVTNCNGCNTTYMGNRTNG 23
 DB 617 GGCTCTCCTCGTTCCGCCGCGG 595
 RESULT 4
 ID AAV00220 standard; DNA; 961 BP.
 AC AAV00220;
 DT 08-JUN-1998 (first entry)
 DE 1-aminocyclopropane-1-carboxylic acid synthase gene acacc3.
 XX 1-aminocyclopropane-1-carboxylic acid; ACC synthase; pineapple;
 KW flowering; inhibition; regulation; development; fruit; ss.
 XX
 OS Ananas comosus.
 XX
 XX Key Location/Qualifiers
 FT 1..961
 FT /tag= a
 FT /product= "acacc3"
 FT /note= "no stop codon given; contains an intron"
 FT 1..101
 FT /tag= b
 FT /number= 1
 FT 102..193
 FT /tag= c
 FT /number= 1
 FT 194..961
 FT /tag= d
 FT /number= 2
 AU9719963-A.
 06-NOV-1997.

XX
 PF 01-MAY-1997; 97AU-0019963.
 XX
 PR 01-MAY-1996; 96AU-0009582.
 XX
 PA (GOLD-) GOLDEN CIRCLE LTD.
 PA (QUE-) STATE QUEENSLAND.
 PA (UYOU) UNIV QUEENSLAND.
 XX
 PI Botella J, Sanewski G;
 XX
 DR WPI: 1998-009279/02.
 DR P-PSDB: AAW37445.
 XX
 PT New isolated ACC synthase genes from pineapples - used to generate
 PT transgenic pineapples in which the natural initiation of flowering
 PT is inhibited
 XX
 PS Claim 2: Fig 2; 37pp; English.
 CC The present sequence represents the nucleotide sequence encoding a
 CC 1-aminocyclopropane-1-carboxylic acid (ACC) synthase enzyme of
 CC pineapple. The present invention describes a transgenic variety of
 CC pineapple in which initiation of flowering is inhibited, the variety
 CC comprising a nucleotide sequence encoding an ACC synthase enzyme where
 CC the nucleotide sequence is operably linked. In the sense or antisense
 CC orientation, to one or more regulatory pineapple plant development.
 CC ACC synthase gene can be used to regulate pineapple plant development.
 CC Particularly for inhibiting initiation of flowering. Such plants can
 CC then be induced to flower in a narrow spectrum of time which would
 CC thereby decrease the spread of fruit maturity within a crop.
 CC
 SO Sequence 961 BP; 235 A; 246 C; 247 G; 233 T; 0 other;
 Query Match
 Best Local Similarity 67.0%; Score 15.4; DB 19; Length 961;
 Matches 13; Conservative 56.5%; Pred. No. 1.5e+02; Indels 0; Gaps 0;
 Mismatches 6;
 OY 1 GGNVTNCNGCNTTYMGNRTNG 23
 DB 567 GGCTACCAAGCTTCCGCCGCGG 589
 RESULT 5
 ID AAV00219 standard; DNA; 968 BP.
 AC AAV00219;
 DT 08-JUN-1998 (first entry)
 DE 1-aminocyclopropane-1-carboxylic acid synthase gene acacc2.
 XX 1-aminocyclopropane-1-carboxylic acid; ACC synthase; pineapple;
 KW flowering; inhibition; regulation; development; fruit; ss.
 XX
 OS Ananas comosus.
 XX
 XX Key Location/Qualifiers
 FT 1..968
 FT /tag= a
 FT /product= "acacc2"
 FT /transl_except= (pos:967..968,aa:Val)
 FT /note= "no stop codon given"
 AU9719963-A.
 06-NOV-1997.
 PF 01-MAY-1997; 97AU-0019963.
 XX
 PR 01-MAY-1996; 96AU-0009582.

PA (GOLD-) GOLDEN CIRCLE LTD.
 PI (OEE-) STATE QUEENSLAND.
 PA (UYOU) UNIV QUEENSLAND.
 XX
 PI Botella J, Sanewski G;
 DR WPI: 1998-009279/02.
 DR P-PSDB: AAW37444.
 XX
 PT New isolated ACC synthase genes from pineapples - used to generate
 PT transgenic pineapples in which the natural initiation of flowering
 PT is inhibited
 PS
 PS Claim 1; Fig 1; 37pp: English.
 XX
 CC The present sequence represents the nucleotide sequence encoding a
 CC 1-aminocyclopropane-1-carboxylic acid (ACC) synthase enzyme of
 CC pineapple. The present invention describes a transgenic variety of
 CC pineapple in which initiation of flowering is inhibited, the variety
 CC comprising a nucleotide sequence encoding an ACC synthase enzyme where
 CC the nucleotide sequence is operably linked, in the sense or antisense
 CC orientation, to one or more regulatory nucleotide sequences. The ACC
 CC synthase gene can be used to regulate pineapple plant development,
 CC particularly for inhibiting initiation of flowering. Such plants can
 CC then be induced to flower in a narrow spectrum of time which would
 CC thereby decrease the spread of fruit maturity within a crop.
 CC
 XX
 SQ Sequence 968 BP; 241 A; 235 C; 294 G; 198 T; 0 other:
 Query Match 67.0%; Score 15.4; DB 19; Length 968;
 Best Local Similarity 56.5%; Pred. No. 1.5e+02;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNYNCCNGNTTYMGNTNG 23
 - || : || || || : || : || ||
 Db 571 GGCTCTCCCGGTTTAGGGTTGG 593

RESULT 6
 AAT73139
 ID AAT73139 standard; cDNA; 993 BP.
 XX
 AC AAT73139;
 XX
 DT 07-DEC-1996 (first entry)
 XX
 DE Broccoli ACC synthase cDNA clone TA13.
 XX
 KW ACC synthase; 1-aminocyclopropyl-1-carboxylic acid synthase;
 KW ethylene; shelf-life; Cucumis melo; melon; transgenic plant;
 KW antisense; broccoli; ss.
 XX
 OS Brassica oleracea.
 XX
 FH Key Location/Qualifiers
 FT mat_peptide 3..992 /tag= a
 FT primer_bind complement (1..14) /tag= b
 FT /note= "primer RMM494"
 FT 975..993 /note= "primer RMM491"
 FT /tag= c
 FT primer_bind
 XX
 PN WO9621027-A1.
 XX
 PD 11-JUL-1996.
 XX
 PD 07-JUN-1995; 95WO-US07271.
 XX
 PF 07-JUN-1995; 95WO-US07271.
 XX
 PR 30-DEC-1994; 94US-0366992.
 XX
 PA (ASGR-) ASGROW SEED CO.
 XX
 PI

XX
 PI Boeshore ML, Carney RJ, Deng RZ, Reynolds JF, Ruttenclutter GE;
 XX
 XX WPI: 1996-334002/33.
 DR P-PSDB: AAR98599.
 DR
 XX
 PT DNA encoding 1-amino:cyclo:propyl-1-carboxylic acid synthase of
 PT Brassica oleracea - used to regulate ethylene-dependent processes
 PT in plants, esp. to improve shelf life
 XX
 PS Claim 3; Fig6A-C; 50pp: English.
 XX
 CC Brassica oleracea cDNA clone TA13 (AAT73137) codes for
 CC 1-aminocyclopropyl-1-carboxylic acid synthase (ACC-synthase)
 CC (AAR98599), an enzyme involved in ethylene biosynthesis. It was
 CC obtd. by PCR amplification (see also AAT73140) of broccoli floret
 CC cDNA. The PCR product was cloned into pCMT1 to obtain clone
 CC TA13. cDNA or genomic DNA (see also AAT73136) can be inserted, in
 CC sense or antisense orientation, into an expression cassette and then
 CC transferred to a binary vector suitable for Agrobacterium-mediated
 CC plant transformation. The constructs permit control of the level of
 CC ACC synthase in a transgenic plant (esp. B. oleracea or Cucumis
 CC melo) and hence a control of maturation, ageing and shelf-life.
 CC
 XX
 SQ Sequence 993 BP; 269 A; 233 C; 253 G; 238 T; 0 other:
 Query Match 67.0%; Score 15.4; DB 17; Length 993;
 Best Local Similarity 56.5%; Pred. No. 1.5e+02;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNYNCCNGNTTYMGNTNG 23
 - || : || || || : || : || ||
 Db 621 GGTCTCTCCCGGTTTCGAGTTGG 643

RESULT 7
 AAT72628
 ID AAT72628 standard; DNA; 1080 BP.
 XX
 AC AAT72628;
 XX
 DT 27-JAN-1998 (first entry)
 XX
 DE Ananas comosus ACC synthase, acaccl gene.
 XX
 KW ACC synthase; S-adenosyl-L-methionine methylthioadenosine lyase;
 KW acaccl; ethylene biosynthesis; transgenic plant; senescence;
 KW antisense expression system; plant development; fruit ripening;
 KW EC 4.4.1.14; pineapple; ss.
 XX
 OS Ananas comosus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1080 /tag= a
 FT /product= acaccl
 FT /EC_number= 4.4.1.14
 FT /note= "Sequence represents 75% of the coding
 FT sequence and does not contain the start
 FT or stop codons."
 XX
 PN WO9711166-A1.
 XX
 PD 27-MAR-1997.
 XX
 PD 20-SEP-1996; 96WO-AU00591.
 XX
 PF 02-MAY-1996; 96AU-0009603.
 XX
 PR 20-SEP-1995; 95AU-0005359.
 XX
 PA (UYOU) UNIV QUEENSLAND.
 XX
 PI Botella JR;
 XX

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XX  WPI: 1997-202875/18.
DR  P-PSDB; AAW18236.
XX
PT  Pineapple, papaya and mango ACC synthase genes - used in gene
XX  therapy to produce fruits with reduced senescence
XX
PS  Claim 1; Fig 1; 46pp; English.
XX
CC  This sequence represents a novel gene, acca1, which encodes an ACC
CC  synthase. The enzyme ACC synthase is involved in the pathway for ethylene
CC  biosynthesis and the rate of endogenous expression of ACC synthase
CC  is considered to limit substantially the rate of ethylene production.
CC  Form of mechanical wounding has occurred and diminishes their post
CC  harvest quality and storage life. Novel ACC synthase genes expressed
CC  in transgenic plants using either sense or antisense expression system
CC  may be used to control the regulation of plant development, in
CC  particular fruit ripening, reducing senescence and thus improving
CC  storage life.
XX
SQ  Sequence 1080 BP; 264 A; 294 C; 299 G; 223 T; 0 other;
Query Match      67.0%; Score 15.4; DB 18; Length 1080;
Best Local Similarity 56.5%; Pred. No. 1.5e+02;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
OY  1 GGNATNCCNGGTTTGMGRNGG 23
    ||:|:|||||:|:|:|:|:|
DB  691 GGTCTCCCGGATTCGAGTCGG 713

RESULT 8
ID  AAT72631 standard; DNA: 1096 BP.
XX
AC  AAT72631;
XX
DT  27-JAN-1998 (first entry)
XX
DE  Mangifera indica ACC synthase miaccl gene.
XX
KM  ACC synthase; S-adenosyl-L-methionine methylthioadenosine lyase;
KM  miaccl; ethylene biosynthesis; transgenic plant; senescence;
KM  antisense expression system; plant development; fruit ripening;
KM  EC 4.4.1.14; mango; multigene family; ss.
XX
OS  Mangifera indica;
XX
FH  Key Location/Qualifiers
FT  CDS 1..1096
FT  /*tag= a
FT  /product= miaccl
FT  /EC_number= 4.4.1.14
FT  /note= "Sequence represents 75% of the coding
FT  sequence and does not contain the start
FT  or stop codons."
XX
PN  WO9711166-A1.
XX
PD  27-MAR-1997.
XX
PF  20-SEP-1996; 36WO-AU00591.
XX
PR  02-MAY-1996; 36AU-0009603.
PR  20-SEP-1995; 35AU-0005559.
XX
PA  (UYOU ) UNTV QUEENSLAND.
XX
PI  Botella JR;
XX
DR  WPI: 1997-202875/18.
DR  P-PSDB; AAW18289.
XX
PT

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```

XX  Pineapple, papaya and mango ACC synthase genes - used in gene
PT  therapy to produce fruits with reduced senescence
XX
PS  Claim 4; Fig 4; 46pp; English.
XX
CC  This sequence represents a novel gene, miaccl, which is a member
CC  of an ACC synthase multigene family found in mango. ACC synthase is
CC  involved in the pathway for ethylene biosynthesis and the rate of
CC  endogenous expression of ACC synthase is considered to limit
CC  substantially the rate of ethylene production. Endogenous ethylene is
CC  often deleterious to crops, especially if some form of mechanical
CC  wounding has occurred and diminishes their post harvest quality and
CC  storage life. Novel ACC synthase genes expressed in transgenic plants
CC  using either sense or antisense expression system may be used to control
CC  the regulation of plant development, in particular fruit ripening,
CC  reducing senescence and thus improving storage life.
XX
SQ  Sequence 1096 BP; 302 A; 227 C; 255 G; 312 T; 0 other;
Query Match      67.0%; Score 15.4; DB 18; Length 1096;
Best Local Similarity 56.5%; Pred. No. 1.6e+02;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
OY  1 GGNATNCCNGGTTTGMGRNGG 23
    ||:|:|||||:|:|:|:|:|
DB  688 GGCCTCCCTGGCTTAGGCTTG 710

RESULT 9
ID  AAT72630 standard; DNA: 1098 BP.
XX
AC  AAT72630;
XX
DT  27-JAN-1998 (first entry)
XX
DE  Carica papaya ACC synthase capacc2 gene.
XX
KM  ACC synthase; S-adenosyl-L-methionine methylthioadenosine lyase;
KM  capacc2; ethylene biosynthesis; transgenic plant; senescence;
KM  antisense expression system; plant development; fruit ripening;
KM  EC 4.4.1.14; papaya; multigene family; ss.
XX
OS  Carica papaya.
XX
FH  Key Location/Qualifiers
FT  CDS 1..1098
FT  /*tag= a
FT  /product= capacc2
FT  /EC_number= 4.4.1.14
FT  /note= "Sequence represents 75% of the coding
FT  sequence and does not contain the start
FT  or stop codons."
XX
PN  WO9711166-A1.
XX
PD  27-MAR-1997.
XX
PF  20-SEP-1996; 96WO-AU00591.
XX
PR  02-MAY-1996; 96AU-0009603.
PR  20-SEP-1995; 95AU-0005559.
XX
PA  (UYOU ) UNTV QUEENSLAND.
XX
PI  Botella JR;
XX
DR  WPI: 1997-202875/18.
DR  P-PSDB; AAW18288.
XX
PT  Pineapple, papaya and mango ACC synthase genes - used in gene
PT  therapy to produce fruits with reduced senescence

```

PS Claim 3; Fig 3; 46pp; English.

XX

CC This sequence represents a novel gene, *capac2*, which is a member
CC of the ACC synthase multigene family found in papaya. The enzyme ACC
CC synthase is involved in the pathway for ethylene biosynthesis and the
CC rate of endogenous expression of ACC synthase is considered to limit
CC substantially the rate of ethylene production. Endogenous ethylene is
CC often deleterious to crops, especially if some form of mechanical
CC wounding has occurred and diminishes their post harvest quality and
CC storage life. Novel ACC synthase genes expressed in transgenic plants
CC using either sense or antisense expression system may be used to control
CC the regulation of plant development, in particular fruit ripening,
CC reducing senescence and thus improving storage life.
XX

SQ Sequence 1098 BP; 276 A; 275 C; 299 G; 248 T; 0 other;

OY Query Match 67.0%; Score 15.4; DB 18; Length 1098;
Best Local Similarity 56.5%; Pred. No.1.6e+02;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0.

Db 1 GGATTCGCGGTTCGCGGTACG 23
||:||| ||||| :||
688 GGTCTCCCCGGTTCCGGGTAGC 710

RESULT 10
AAT72629
ID AAT72629 standard; DNA; 1104 BP.

AC AAT72629;

DX 27-JAN-1998 (first entry)

XX

DE Carica papaya ACC synthase *capac1* gene.

XX

KM ACC synthase: S-adenosyl-L-methionine methylthioadenosine lyase;
KM *capac1*; ethylene biosynthesis; transgenic plant; senescence;
KM antisense expression system; plant development; fruit ripening;
KM EC 4.4.1.14; papaya; multigene family; ss.

OS Carica papaya.

XX

FH Key Location/Qualifiers
FT 1..1104
FT /*tag= a
FT /EC_number= 4.4.1.14
FT /product= *capac1*
FT /note= "Sequence represents 75% of the coding
FT sequence and does not contain the start
FT or stop codons."

CDS

XX

PN WO9711166-A1.

XX

PD 27-MAR-1997 .

XX

Pf 20-SEP-1996; 96MO-AU00591.

XX

PR 02-MAY-1996; 96AU-0009603.
PR 20-SEP-1995; 95AU-0005559.

XX

PA (UYOU) UNIV QUEENSLAND.

XX

PI Botella JR;

XX

DR WPI; 1997-202875/18.
DR P-PDB; AA018287.

XX

PT Pineapple, papaya and mango ACC synthase genes - used in gene
PT therapy to produce fruits with reduced senescence
XX
XX Claim 2; Fig 2; 46pp; English.
XX

CC	This sequence represents a novel gene, caccpccl1, a member of the papaya ACC synthase multigene family. ACC synthase is an enzyme involved in the pathway for ethylene biosynthesis and the rate of endogenous expression of ACC synthase is considered to limit substantially the rate of ethylene production. Endogenous ethylene is often deleterious to crops, especially if some form of mechanical wounding has occurred and diminishes their post harvest quality and storage life. Novel ACC synthase genes expressed in transgenic plants using either sense or antisense expression system may be used to control the regulation of plant development, in particular fruit ripening, reducing senescence and thus improving storage life.
CC	
XX	
SQ	Sequence 1104 BP; 325 A; 214 C; 257 G; 308 T; 0 other:
OY	Query Match 67.0%; Score 15.4; DB 18; Length 1104; Best Local Similarity 56.5%; Pred. No. 1.6e+02;
DB	Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
	1 GGNYTNCNGNMTYMGNRTGCG 23 : : Db GGATTCCTCAGATTACAGATTGC 719
RESULT 11	
AAT72632	ID AAT72632 standard; DNA; 1113 BP.
XX AC	AAT72632;
XX XX	27-JAN-1998 (first entry)
DE DE	Mangifera indica ACC synthase miacc2 gene.
XX KM	ACC synthase; S-adenosyl-L-methionine methyltransferase lyase; miacc2; ethylene biosynthesis; transgenic plant; senescence; antisenese expression system; plant development; fruit ripening; EC 4.4.1.14; mango; multigenic family; ss.
OS OS	Mangifera indica.
XX FH	Key Location/Qualifiers
FT FT	CDS 1..1113
FT FT	/*tag= a
FT FT	/EC number= 4.4.1.14
FT FT	/product= miacc2
FT FT	/note= "sequence represents 75% of the coding sequence and does not contain the start or stop codons."
PN PN	WO9711166-A1.
XX PD	27-MAR-1997.
XX PF	20-SEP-1996; 96WU-AU00591.
XX PR	02-MAY-1996; 96AU-0009603.
PR PA	20-SEP-1995; 95AU-0005559.
XX PI	(UYQU) UNIV QUEENSLAND.
XX PT	Botella JR;
DR DR	WIPI: 1997-202875/18.
P-PADB; AAHI8290.	
XX PX	Pineapple, papaya and mango ACC synthase genes - used in gene therapy to produce fruits with reduced senescence
PS PS	Claim 5; Fig 5; 46pp; English.
CC CC	This sequence represents the novel gene, miacc2, which is a member of the mango ACC synthase multigene family. ACC synthase is an enzyme involved in the pathway for ethylene biosynthesis and the rate of

CC plant transformation. The constructs permit control of the level of
CC ACC synthase in a transgenic plant (esp. B. oleracea or Cucumis
CC melo) and hence a control of maturation, ageing and shelf-life.
XX

SO Sequence 1384 BP; 401 A; 290 C; 310 G; 383 T; 0 other;

Query Match 67.0%; Score 15.4; DB 17; Length 1384;
Best Local Similarity 56.5%; Pred. No. 1.6e+02;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNVTNCCNGNTTYMGNRTNG 23
DB 970 GGCTTCCCGGTTTCGAGTTGG 992

RESULT 14
AAQ25896
ID AAQ25896 standard; cDNA; 1482 BP.

XX AAQ25896;

XX 18-JAN-1993 (first entry)

XX ACC synthetase gene.

XX I-aminocyclopropane-1-carboxylic acid synthetase; detriment;

XX ethylene; growth; maturity; aging; plant; ss.

XX Cucurbita maxima.

XX JF04169183-A.

XX 17-JUN-1992.

XX 31-OCT-1990; 90JP-0296943.

XX 31-OCT-1990; 90JP-0296943.

XX (SUMO) SUMITOMO CHEM CO LTD.

XX WPI: 1992-253389/31.

XX P-PSDB; AAR25406.

XX Detriment induced ACC synthetase gene - used for control of

XX bio-synthesis of ethylene, for controlling growth, maturity and

XX ageing of higher plant

XX Claim 3; Fig 1; 10pp; Japanese.

XX The gene encoding detriment induced 1-aminocyclopropane-1-carboxylic

XX acid (ACC) synthetase (EC 4.4.1.14) was obtd. by screening a cDNA

XX library prepd. from Cucurbita maxima mRNA. EC4.4.1.14 obtd. from

XX cDNA library clones was screened by an antibody method to identify

XX colonies producing EC 4.4.1.14, e.g. E.coli DH5 alpha/PCMW33.

XX Biosynthesis of ethylene is controlled by ACC synthetase. Ethylene

XX controls the growth, maturing and aging of higher plants.

XX Sequence 1482 BP; 415 A; 341 C; 344 G; 382 T; 0 other;

XX Query Match 67.0%; Score 15.4; DB 13; Length 1482;

XX Best Local Similarity 56.5%; Pred. No. 1.6e+02;

XX Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

XX OY 1 GGNVTNCCNGNTTYMGNRTNG 23

XX DB 844 GGCTTCCCGGTTTCGAGTTGG 866

XX 17-DEC-2001 (updated)

XX 09-MAR-1992 (first entry)

XX Clone pACC1 encoding the Zucchini ACC synthase.

XX 1-aminocyclopropane-1-carboxylic acid synthase; fruit ripening;

XX courgette; ss.

XX Cucurbita pepo.

XX key Location/Qualifiers

XX CDS 11..1492

XX /tag= a

XX /EC_number= 4.4.1.14

XX misc_signal 1683..1688

XX /tag= b

XX USN7579896-N.

XX 12-NOV-1991.

XX 10-SEP-1990; 90US-0579896.

XX 10-SEP-1990; 90US-0579896.

XX (USDA) US SEC OF AGRICULTURE.

XX Theologis A, Sato T;

XX WPI: 1991-368895/50.

XX P-PSDB; AAR15504.

XX DNA encoding ACC synthase - used for control of plant development

XX and for prodn. of ACC synthase, ethylene and ethanol

XX Disclosure: Fig 1B; 73pp; English.

XX The ACC synthase cDNA was isolated from C.pepo using a novel method.

XX A cDNA expression library was prepared from induced plant tissue.

XX The library was screened with an antibody preparation obtained by

XX partially purifying the induced ACC synthase and using it to

XX immunise a suitable mammal. Immunoreactive clones were isolated and

XX sequenced. One of these, pACC1, contained an open reading frame

XX corresponding to a protein of 493 amino acids and mol. wt.

XX 55,779 kD. See also AAQ5132-015140.

XX (Note: Revised entry submitted to correct the patent number format of

XX US Government-owned NTIS applications to prevent clashes with ongoing US

XX granted patent numbers. For further information please visit the Derwent

XX web site at www.derwent.com/dwpl/updates/ntis-us.html.)

XX Sequence 1703 BP; 481 A; 359 C; 378 G; 485 T; 0 other;

XX Query Match 67.0%; Score 15.4; DB 12; Length 1703;

XX Best Local Similarity 56.5%; Pred. No. 1.6e+02;

XX Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

XX OY 1 GGNVTNCCNGNTTYMGNRTNG 23

XX DB 854 GGCTTCCCGGTTTCGAGTTGG 876

XX Search completed: March 10, 2003, 05:25:14

XX Job time: 179.5 secs


```

FT      /tag= e
FT      /mod_base= i
XX
XX      WO9814465-A1.
XX
XX      09-APR-1998.
XX
XX      30-SEP-1997; 97WO-US17644.
XX
XX      01-OCT-1996; 96US-0724194.
XX
XX      (COLS ) UNIV COLORADO STATE RES FOUND.
XX
XX      Ranu RS:
XX      WPI: 1998-260994/23.
XX
XX      New isolated ACC synthase genes - are obtained from geranium and
XX      rose, used to develop products for producing plants with reduced
XX      ethylene levels, for increasing shelf-life
XX
XX      Example: Page 37; 77pp; English.
XX
XX      Primer II and primer I (see AAV30328) were used in PCR amplifications
XX      to develop PCR probes for the isolation of geranium and rose
XX      1-aminocyclopropane-1-carboxylate synthase (ACC synthase) cDNA
XX      clones (See AAV30324-26 and AAV30330). The invention relates to the
XX      use of antisense fragments of these genes to control ACC synthase
XX      expression in plants. By reducing the amount of ACC synthase
XX      produced in plant cells, the rate of ACC conversion to ethylene
XX      can be decreased. This can be used to prolong the shelf-life of
XX      cut flowers and to reduce leaf yellowing and petal abscission
XX      during shipping and storage.
XX
XX      Sequence 23 BP; 5 A; 5 C; 0 G; 1 T; 12 other:
XX
XX      Query Match      66.1%; Score 15.2; DB 19; Length 23;
XX      Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX      Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY      1 CANANNCCKRAASMANCCNRSYTC 23
      ||||||||||||||||||
Db      1 CANANNCCKRAASMANCCNRSYTC 23

RESULT 2
AAS19699
ID      AAS19699 standard; DNA; 23 BP.
XX
XX      AAS19699;
XX
XX      09-APR-2002 (first entry)
XX
XX      PCR primer #2 used to amplify DNA fragment of geranium PHSacc genes.
XX
XX      Geranium: 1-aminocyclopropane-1-carboxylate synthase gene promoter;
XX      ACC synthase; plant transcription regulation; plant; PCR; primer;
XX      gPHSacc49; ss.
XX
XX      pelargonium x hortorum.
XX
XX      WO200185754-A1.
XX
XX      15-NOV-2001.
XX
XX      09-MAY-2001; 2001WO-US15023.
XX
XX      09-MAY-2000; 2000US-203021P.
XX      12-OCT-2000; 2000US-239782P.
XX
XX      (COLS ) UNIV COLORADO STATE.
XX      (TAGA-) TAGAWA GREENHOUSES INC.
XX

```

```

PI      Ranu RS:
XX
XX      WPI: 2002-075241/10.
XX
XX      New promoter from the 1-aminocyclopropane-1-carboxylase synthase gene
XX      of geranium, useful to regulate level of transcription of coding
XX      sequence in geranium and other plants -
XX
XX      Claim 7; Fig 2; 38pp; English.
XX
XX      The present invention relates to the isolation of promoter DNA from
XX      geranium (pelargonium x hortorum) genomic clone gPHSacc49 (gPHSacc49).
XX      This promoter represents the ACC (1-aminocyclopropane-1-carboxylate)
XX      synthase gene promoter. The promoter is useful to regulate the
XX      transcription level of a coding sequence in geranium and other plants.
XX      The present sequence represents a PCR primer used to amplify a DNA
XX      fragment of geranium PHSacc genes.
XX
XX      Sequence 23 BP; 5 A; 5 C; 0 G; 1 T; 12 other:
XX
XX      Query Match      66.1%; Score 15.2; DB 24; Length 23;
XX      Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX      Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY      1 CANANNCCKRAASMANCCNRSYTC 23
      ||||||||||||||||||
Db      1 CANANNCCKRAASMANCCNRSYTC 23

RESULT 3
ABQ65439
ID      ABQ65439 standard; DNA; 748 BP.
XX
XX      ABQ65439;
XX
XX      21-AUG-2002 (first entry)
XX
XX      Arabidopsis thaliana polynucleotide seq ID NO 16.
XX
XX      Arabidopsis thaliana; thale cress; plant; transgenic; GMO; disease;
XX      stress; metabolic pathway; biosynthetic pathway; nutrition; fungicide;
XX      insecticide; antibiotic; ds.
XX
XX      Arabidopsis thaliana.
XX
XX      US2002059663-A1.
XX
XX      16-MAY-2002.
XX
XX      26-JAN-2001; 2001US-0770149.
XX
XX      27-JAN-2000; 2000US-178506P.
XX
XX      (GORL/) GORLACH J.
XX      (ANY/) AN Y.
XX      (HANT/) HAMILTON C M.
XX      (PRIC/) PRICE J L.
XX      (RAIN/) RAINES T M.
XX      (YUY/) YU Y.
XX      (RAME/) RAMEAKA J G.
XX      (PAGE/) PAGE A.
XX      (MATH/) MATHEW A V.
XX      (LEDE/) LEDFORD B L.
XX      (WOES/) WOESSNER J P.
XX      (HAAS/) HAAS W D.
XX      (GARC/) GARCIA C A.
XX      (KRIC/) KRICKER M.
XX      (SLAT/) SLATER T.
XX      (DAVI/) DAVIS K R.
XX      (ALLE/) ALLEN K.
XX      (HOFF/) HOFFMAN N.
XX      (HURE/) HURBAN P.
XX

```

PI Gorlach J, An Y, Hamilton CM, Price JL, Raines JM, Yu Y;
 PI Rameaux JE, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
 PI Garcia CA, Krieger M, Slater T, Davis KR, Allen K, Hoffman N;
 PI Hurban P;
 DR WPI: 2002-4792:4/51.
 XX
 XX
 PT New nucleic acid that hybridizes to Arabidopsis thaliana sequences,
 PT useful e.g. for preparing transgenic plants with increased resistance
 PT or altered metabolism
 PS
 XX Claim 1: SEQ ID NO 16; 40pp + Sequence Listing; English.
 CC The invention relates to nucleic acids (I) that hybridise under stringent
 CC conditions to any of 999 sequences (AB05424-AB06422) or their
 CC fragments (II) and used to express the corresponding polypeptides (III) or
 CC to produce genetically modified plant cells or transgenic plants, which
 CC may have improved resistance to disease or stress, or altered
 CC metabolic/biosynthetic pathways (for production of commercial,
 CC nutritional or medicinal products), or generally any trait of interest,
 CC or can be used to screen for biologically active agents (e.g. fungicides,
 CC insecticides and antibiotics).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC USPTO at seqdata.uspto.gov/sequence.html?docID=999909770149.
 CC
 SQ Sequence 748 BF: 209 A; 202 C; 120 G; 213 T; 4 other;
 Query Match 66.1%; Score 15.2; DB 24; Length 748;
 Best Local Similarity 47.8%; Pred. No. 2.8e+02;
 Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 OY 1 CANANNCRRASMANCNRSYTC 23
 DB 217 CAACCCCTAAACCATCGACCTC 239
 ID AAT38897 standard; cDNA; 1087 BP.
 AC AAT38897;
 XX
 XX 10-FEB-1997 (first entry)
 DE Carnation ACC synthase gene fragment.
 XX
 XX Carnation; 1-aminocyclopentane-1-carboxylic acid synthase;
 KM ACC synthase; co-suppression; ethylene; senescence;
 KM transgenic plant; ss.
 XX
 XX Dianthus sp. cv. White Sin.
 OS
 XX
 PN W09635792-A1.
 XX
 PD 14-NOV-1996.
 XX
 PF 09-MAY-1996; 36MO-AU00286.
 XX
 PR 09-MAY-1995; 35AU-0002862.
 XX
 PA (ALLR-) ALLRAD NO 1 PTY LTD.
 PA (FLOR-) FLORIGENE INVESTMENTS PTY LTD.
 XX
 PI Cornish EC, Graham MW, Guttererson NI, Michael MZ;
 PI Tucker WT;
 DR WPI: 1996-51868/51.
 DR P-PSDB: AAW04553.
 PT Producing transgenic plants, with reduced climacteric ethylene
 PT prodn. - to give flowers and buds, specifically carnations, with
 PT increased post-harvest life

XX Claim 10: Page 42-44; 98pp; English.
 PS
 XX A non full-length gene (AAT38897) comprises nucleotides 287-1373 of
 CC a 1-aminocyclopentane-1-carboxylic acid (ACC) synthase gene
 CC (AAT38896) isolated from carnation cv. White Sin. It was obtd. by
 CC PCR amplification of carnation cDNA using primers (AAT38899-900)
 CC based on highly conserved regions of the ACC synthase gene.
 CC Transgenic carnation plants carrying the non full-length gene show
 CC reduced prodn. of ACC synthase or ACC synthase-specific mRNA as a
 CC result of co-suppression. This leads to decreased climacteric
 CC ethylene prodn. by the plant and hence delayed senescence of
 CC flowers and buds after cutting, and increased post-harvest life.
 CC
 SQ Sequence 1087 BF: 309 A; 204 C; 251 G; 323 T; 0 other;
 Query Match 66.1%; Score 15.2; DB 17; Length 1087;
 Best Local Similarity 47.8%; Pred. No. 3e+02;
 Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 OY 1 CANANNCRRASMANCNRSYTC 23
 DB 1085 CAACCCCTAAACCAACCCGCGCTC 1063
 ID AAT72631/C
 XX AAT72631 standard; DNA; 1096 BP.
 AC AAT72631;
 XX
 XX 27-JAN-1998 (first entry)
 DE Mangifera indica ACC synthase mlacl1 gene.
 XX
 XX Mangifera indica ACC synthase mlacl1 gene.
 KM ACC synthase; S-adenosyl-L-methionine methylthiodenosine lyase;
 KM mlacl1; ethylene biosynthesis; transgenic plant; senescence;
 KM antisense expression system; plant development; fruit ripening;
 KM EC 4.4.1.14; mango; multigene family; ss.
 XX
 OS Mangifera indica.
 XX
 FH Key Location/Qualifiers
 FT 1..1096
 FT CDS
 FT /**tag= 3
 FT /product= mlacl1
 FT /EC_number= 4.4.1.14
 FT /note= "Sequence represents 75% of the coding
 FT sequence and does not contain the start
 FT or stop codons."
 XX
 PN W09711166-A1.
 XX
 PD 27-MAR-1997.
 XX
 PF 20-SEP-1996; 96MO-AU00591.
 XX
 PR 02-MAY-1996; 96AU-0009603.
 XX
 PR 20-SEP-1995; 95AU-0005559.
 XX
 PA (UYOU) UNIV QUEENSLAND.
 PA Botella JR;
 XX
 PI WPI: 1997-202875/18.
 DR P-PSDB: AAW18289.
 XX
 XX Pineapple, papaya and mango ACC synthase genes - used in gene
 XX therapy to produce fruits with reduced senescence
 PS Claim 4: Fig 4; 46pp; English.
 XX
 XX This sequence represents a novel gene, mlacl1, which is a member

CC of an ACC synthase multigene family found in mango. ACC synthase is
CC involved in the pathway for ethylene biosynthesis and the rate of
CC endogenous expression of ACC synthase is considered to limit
CC substantially the rate of ethylene production. Endogenous ethylene is
CC often deleterious to crops, especially if some form of mechanical
CC wounding has occurred and diminishes their post harvest quality and
CC storage life. Novel ACC synthase genes expressed in transgenic plants
CC using either sense or antisense expression system may be used to control
CC the regulation of plant development, in particular fruit ripening,
CC reducing senescence and thus improving storage life.

XX
SQ Sequence 1096 BP; 302 A; 227 C; 255 G; 312 T; 0 other;

Query Match 66.1%; Score 15.2; DB 18; Length 1096;
Best Local Similarity 47.8%; Pred. No. 3e+02;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 CANANCKRASMNCNRSYTC 23
|||1::||:|1|::|1|
Db 1088 CAGACTCTGAAACCAACGAGCTC 1066

RESULT 6
AAT72630/C
ID AAT72630 standard; DNA; 1098 BP.
XX
AC AAT72630;
XX
DT 27-JAN-1998 (first entry)
XX
DE Carica papaya ACC synthase capacc2 gene.
XX
KW ACC synthase; S-adenosyl-L-methionine methylthioadenosine lyase;
KW capacc2; ethylene biosynthesis; transgenic plant; senescence;
KW antisense expression system; plant development; fruit ripening;
KW EC 4.4.1.14; papaya; multigene family; ss.
XX
OS Carica papaya.
XX
FH Key Location/Qualifiers
FT CDS 1..1098
FT /*tag= a
FT /EC_number= 4.4.1.14
FT /product= capacc2
FT /note= "Sequence represents 75% of the coding
FT sequence and does not contain the start
FT or stop codons."

XX
PM WO9711166-A1.
XX
PD 27-MAR-1997.
XX
XX
PF 20-SEP-1996; 96MO-AU00591.
XX
XX
PR 02-MAY-1996; 96AU-0009603.
PR 20-SEP-1995; 95AU-0005559.
XX
XX
PA (UYOU) UNIV QUEENSLAND.
XX
XX
PI Botella JR.
XX
XX WPI: 1997-202875/18.
DR P-PSDB: AAW18288.
XX
XX
XX
PT Pineapple, papaya and mango ACC synthase genes - used in gene
PT therapy to produce fruits with reduced senescence
XX
XX
PS Claim 3; Fig 3; 46pp; English.

CC This sequence represents a novel gene, capacc2, which is a member
CC of the ACC synthase multigene family found in papaya. The enzyme ACC
CC synthase is involved in the pathway for ethylene biosynthesis and the
CC rate of endogenous expression of ACC synthase is considered to limit

CC substantially the rate of ethylene production. Endogenous ethylene is
CC often deleterious to crops, especially if some form of mechanical
CC wounding has occurred and diminishes their post harvest quality and
CC storage life. Novel ACC synthase genes expressed in transgenic plants
CC using either sense or antisense expression system may be used to control
CC the regulation of plant development, in particular fruit ripening,
CC reducing senescence and thus improving storage life.

XX
SQ Sequence 1098 BP; 276 A; 275 C; 299 G; 248 T; 0 other;

Query Match 66.1%; Score 15.2; DB 18; Length 1098;
Best Local Similarity 47.8%; Pred. No. 3e+02;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 CANANCKRASMNCNRSYTC 23
|||1::||:|1|::|1|
Db 1091 CATACTCTGAAACCAACCGGCTC 1069

RESULT 7
AAT72629/C
ID AAT72629 standard; DNA; 1104 BP.
XX
AC AAT72629;
XX
DT 27-JAN-1998 (first entry)
XX
DE Carica papaya ACC synthase capacc1 gene.
XX
XX
KW ACC synthase; S-adenosyl-L-methionine methylthioadenosine lyase;
KW capacc1; ethylene biosynthesis; transgenic plant; senescence;
KW antisense expression system; plant development; fruit ripening;
KW EC 4.4.1.14; papaya; multigene family; ss.
XX
OS Carica papaya.
XX
FH Key Location/Qualifiers
FT CDS 1..1104
FT /*tag= a
FT /EC_number= 4.4.1.14
FT /product= capacc1
FT /note= "Sequence represents 75% of the coding
FT sequence and does not contain the start
FT or stop codons."

XX
PM WO9711166-A1.
XX
PD 27-MAR-1997.
XX
XX
PF 20-SEP-1996; 96MO-AU00591.
XX
XX
PR 02-MAY-1996; 96AU-0009603.
PR 20-SEP-1995; 95AU-0005559.
XX
XX
PA (UYOU) UNIV QUEENSLAND.
XX
XX
PI Botella JR.
XX
XX WPI: 1997-202875/18.
DR P-PSDB: AAW18287.
XX
XX
XX
PT Pineapple, papaya and mango ACC synthase genes - used in gene
PT therapy to produce fruits with reduced senescence
XX
XX
PS Claim 2; Fig 2; 46pp; English.

CC This sequence represents a novel gene, capacc1, a member of the papaya
CC ACC synthase multigene family. ACC synthase is an enzyme involved in
CC the pathway for ethylene biosynthesis and the rate of endogenous
CC expression of ACC synthase is considered to limit substantially the rate
CC of ethylene production. Endogenous ethylene is often deleterious to
CC crops, especially if some form of mechanical wounding has occurred and
CC diminishes their post harvest quality and storage life. Novel ACC

CC synthase genes expressed in transgenic plants using either sense or
CC antisense expression system may be used to control the regulation of
CC plant development, in particular fruit ripening, reducing senescence and
CC thus improving storage life.
XX
SQ Sequence 1104 BP; 325 A; 214 C; 257 G; 308 T; 0 other;
Query Match 66.1%; Score 15.2; DB 18; Length 1104;
Best Local Similarity 47.8%; Pred. No. 3e+02; Mismatches 7; Indels 0; Gaps 0;
Matches 11; Conservative 5; Indels 0; Gaps 0;
QY 1 CANANCKRAASMANCNRSTYC 23
DB 1097 CAGACGCTGACACGACGAGTTC 1075
RESULT 8
AAH77094/C ID AAH77094 standard; cDNA; 1154 BP.
XX
AC AAH77094;
XX
DT 15-DEC-2001 (first entry)
XX
DE Human ATP-dependent serine proteinase 31-encoding cDNA.
XX
KW Human; ATP-dependent serine proteinase 31; recombinant production;
KW malignant tumor; cancer; blood disease; HIV infection;
KW human immunodeficiency virus; immune disorder; inflammatory condition;
KW cytosolic; anti-HIV; antiinflammatory; immunomodulator; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 128..985
FT /ftag="a
FT /product="Human ATP-dependent serine proteinase 31"
XX
XX MO200175125-A1.
XX
PD 11-OCT-2001.
XX
PF 23-MAR-2001; 2001WO-CN00405.
XX
PR 24-MAR-2000; 2000CN-0115085.
XX
PA (SHAN-) SHANGHAI BOWINDON GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
PI WPI: 2001-626440/72.
XX
DR P-PSDB; AAG66837.
XX
XX Human adenovine triphosphate dependent serine proteinase 31 and encoded
PT polynucleotide, applicable in diagnosis and treatment of malignant
PT tumor, hemopathy, human immunodeficiency virus infection, immunological
PT diseases and inflammation
XX
PS Claim 6; Page 33-31; 36pp; Chinese.
XX
CC This sequence represents cDNA encoding human ATP-dependent serine
CC proteinase 31. The protein has a molecular weight of 31 kD. The invention
CC relates to human ATP-dependent serine proteinase 31 (AAG66837), nucleic
CC acids encoding it (AAH77094), and a method for the recombinant production
CC of ATP-dependent serine proteinase 31. The present invention additionally
CC discloses an antagonist of ATP-dependent serine proteinase 31 for
CC therapeutic use, and an antibody which specifically binds to ATP-
CC dependent serine proteinase 31. ATP-dependent serine proteinase 31, and
CC nucleotides which encode it may be used for treating a variety of
CC diseases, such as malignant tumours, blood diseases, HIV (human
CC immunodeficiency virus) infection, immune disorders and inflammatory
CC conditions. The protein may also be used to screen for modulators of its
CC activity or for peptide fingerprinting identification. The polynucleotide

CC can be used as a primer for nucleic acid amplification reactions or as a
CC probe for hybridisation reactions, or in producing gene chips or
CC microarrays.
XX
SQ Sequence 1154 BP; 302 A; 228 C; 290 G; 334 T; 0 other;
Query Match 66.1%; Score 15.2; DB 22; Length 1154;
Best Local Similarity 47.8%; Pred. No. 3e+02; Mismatches 7; Indels 0; Gaps 0;
Matches 11; Conservative 5; Indels 0; Gaps 0;
QY 1 CANANCKRAASMANCNRSTYC 23
DB 174 CAGAGACGAGAGACGACGAGCTC 152
RESULT 9
AAT66247/C ID AAT66247 standard; DNA; 1170 BP.
XX
AC AAT66247;
XX
DT 28-JUL-1997 (first entry)
XX
DE ACC synthase GAC-2 DNA.
XX
DE ACC synthase: 1-aminocyclopropane-1-carboxylate synthase; antisense;
KW ACC synthase: 1-aminocyclopropane-1-carboxylate synthase; antisense;
KW ethylene; transgenic plant; Pelargonium x domesticum;
KW in vitro propagation; tissue culture; ripening; ss.
XX
OS Not identified.
XX
XX W09717429-A1.
XX
XX 15-MAY-1997.
XX
PD 08-NOV-1996; 96WO-US17954.
XX
PF 09-NOV-1995; 95US-0555755.
XX
PR (OGLE-) OGLEVEE LTD.
XX
PA (PENN-) PENN STATE RES FOUND.
XX
XX Arteca J, Arteca RN, Oglevee-O'Donovan W, Stools E;
XX
PI WPI: 1997-281019/25.
XX
DR P-PSDB; AAM09879.
XX
XX Commercial propagation of transgenic plants by tissue culture -
PT especially Pelargonium x domesticum with decreased ethylene
PT formation
XX
PS Claim 14; Page 24; 36pp; English.
XX
XX 2 DNA sequences (AAT66246-47) respectively code for
CC 1-aminocyclopropane carboxylase synthases (ACC synthase) GAC-1
CC (AAM09878) and GAC-2 (AAM09879), enzymes involved in the biosynthesis
CC of ethylene in plants. In a method for the commercial production
CC of transgenic plants, Agrobacterium vectors carrying antisense
CC genes for ACC synthase or ACC oxidase (see also AAT66248) are used
CC to inoculate petiole explants of a mother plant, pref.
CC Pelargonium x domesticum. The resulting callus is cultured and
CC used to regenerate transgenic plants. The antisense genes prevent
CC ACC synthase or ACC oxidase expression and hence ethylene
CC formation and fruit ripening.
XX
SQ Sequence 1170 BP; 319 A; 263 C; 297 G; 291 T; 0 other;
Query Match 66.1%; Score 15.2; DB 18; Length 1170;
Best Local Similarity 47.8%; Pred. No. 3e+02; Mismatches 7; Indels 0; Gaps 0;
Matches 11; Conservative 5; Indels 0; Gaps 0;
QY 1 CANANCKRAASMANCNRSTYC 23
DB 174 CAGAGACGAGAGACGACGAGCTC 152

```

Db      1163 CAGACTCTGAACCAACCTGGCTC 1141

RESULT 10
AAQ25896/c
ID      AAQ25896 standard; cDNA: 1482 BP.
XX
XX      AAQ25896;
AC
XX      18-JAN-1993 (first entry)
DT
XX
XX      ACC synthetase gene.
DE
XX      1-aminocyclopropane-1-carboxylic acid synthetase; detriment;
KW      ethylene; growth; maturity; aging; plant; ss.
XX
XX      Cucurbita maxima.
OS
XX      JP04169183-A.
PN
XX      17-JUN-1992.
PD
XX      31-OCT-1990; 90JP-0296943.
PF
XX      31-OCT-1990; 90JP-0296943.
PR
XX      31-OCT-1990; 90JP-0296943.
PS
XX      (SUMO ) SUMITOMO CHEM CO LTD.
PA
XX      WPI; 1992-253389/31.
DR
XX      P-PSDB; AAR25406.
XX
XX      Detriment induced ACC synthetase gene - used for control of
PT      bio-synthesis of ethylene, for controlling growth, maturity and
PR      ageing of higher plant
PS
XX      Claim 3; Fig 1; 10pp; Japanese.
XX
XX      The gene encoding detriment induced 1-aminocyclopropane-1-carboxylic
CC      acid (ACC) synthetase (EC 4.4.1.14) was obtd. by screening a cDNA
CC      library prepd. from Cucurbita maxima mRNA. EC4.4.1.14 obtd. from
CC      cDNA library clones was screened by an antibody method to identify
CC      clones producing EC 4.4.1.14, e.g. E.coli DH5 alpha/PCMW33.
CC      Biosynthesis of ethylene is controlled by ACC synthetase. Ethylene
CC      controls the growth, maturing and aging of higher plants.
XX
XX      Sequence 1482 BP; 415 A; 341 C; 344 G; 382 T; 0 other;
SQ
Query Match      66.1%; Score 15.2; DB 13; Length 1482;
Best Local Similarity 47.8%; Pred. No. 3.1e+02;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY      1 CANANCKRRAAMNCNRSYTC 23
      || | |::|::| | |::| |
Db      1244 CAAACTCGAACCACCTGGCTC 1222

RESULT 11
AAQ15131/c
ID      AAQ15131 standard; cDNA: 1703 BP.
XX
XX      AAQ15131;
AC
XX      17-DEC-2001 (updated)
DT
XX      09-MAR-1992 (first entry)
DE
XX      Clone PAC1 encoding the Zucchini ACC synthase.
XX
XX      1-aminocyclopropane-1-carboxylic acid synthase; fruit ripening;
KW      courgette; ss.
XX
XX      Cucurbita pepo.
OS
XX
XX      Key      Location/Qualifiers
FH
XX

```

```

FT      CDS      11..1492
FT      /*tag= a
FT      /EC_number= 4.4.1.14
FT      misc_signal
FT      1683..1688
FT      /*tag= b

USN7579896-N.
XX
XX      12-NOV-1991.
PD
XX
XX      10-SEP-1990; 90US-0579896.
PF
XX      10-SEP-1990; 90US-0579896.
PR
XX      10-SEP-1990; 90US-0579896.
PS
XX      (USDA ) US SEC OF AGRICULTURE.
PA
XX      Theologis A, Sato T;
XX
XX      WPI; 1991-368895/50.
DR
XX      P-PSDB; AAR15504.
XX
XX      DNA encoding ACC synthase - used for control of plant development
PT      and for prodn. of ACC synthase, ethylene and ethanol
PR
XX
XX      Disclosure; Fig 1B; 73pp; English.
PS
XX
XX      The ACC synthase cDNA was isolated from C.pepo using a novel method.
CC      A cDNA expression library was prepared from induced plant tissue.
CC      The library was screened with an antibody preparation obtained by
CC      partially purifying the induced ACC synthase and using it to
CC      immunise a suitable mammal. Immunoreactive clones were isolated and
CC      sequenced. One of these, PAC1, contained an open reading frame
CC      corresponding to a protein of 493 amino acids and mol. wt.
CC      55.779 kD. See also AAQ15132-015140.
CC      (Note: Revised entry submitted to correct the patent number format of
CC      US Government-owned NTS applications to prevent clashes with ongoing US
CC      granted patent numbers. For further information please visit the Derwent
CC      web site at www.derwent.com/dwpi/updates/ntis.us.html.)
XX
XX      Sequence 1703 BP; 481 A; 359 C; 378 G; 485 T; 0 other;
SQ
Query Match      66.1%; Score 15.2; DB 12; Length 1703;
Best Local Similarity 47.8%; Pred. No. 3.2e+02;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY      1 CANANCKRRAAMNCNRSYTC 23
      || | |::|::| | |::| |
Db      1254 CAAACTCGAACCACCTGGCTC 1232

RESULT 12
AAV15701/c
ID      AAV15701 standard; cDNA: 1703 BP.
XX
XX      AAV15701;
AC
XX      01-JUN-1998 (first entry)
DT
XX
XX      Zucchini ACC synthase clone PAC1.
DE
XX
XX      Zucchini; courgette; ACC synthase; conserved peptide; clone PAC1;
KW      1-aminocyclopropane-1-carboxylic acid synthase;
XX      delayed fruit ripening; transgenic plant; ss.
XX
XX      Cucurbita pepo.
OS
XX
XX      Key      Location/Qualifiers
FH
XX      CDS      11..1492
FT      /*tag= a
FT      /product= ACC-synthase
XX
XX      US5723766-A.
XX

```

PD 03-MAR-1998.
 XX
 PF 07-JUN-1995; 95US-0481171.
 XX
 PR 02-APR-1992; 92US-0862493.
 XX
 PR 10-SEP-1990; 90US-0579896.
 PR 25-JAN-1995; 95US-0378313.
 PR 07-JUN-1995; 95US-0481171.
 XX
 PA (USDA) US SEC OF AGRIC.
 XX
 PI Sato T, Theologis A;
 XX
 DR WPI: 1998-2060C5/18.
 DR P-PSDB: AAW47310;
 XX
 PT DNA encoding anti-sense RNA blocking plant ACC synthase expression -
 XX
 XX is used for producing transgenic plants with delayed fruit ripening -
 XX
 XX Example 1; Column 33-38; 91pp; English.
 XX
 CC The present sequence is the zucchini
 CC 1-aminocyclopropane-1-carboxylic acid (ACC) synthase clone PACCl.
 CC PACCl was used for the isolation of conserved sequences from five
 CC tomato LE-ACC 1, LE-ACC 1b, LE-ACC 2, LE-ACC 3, and LE-ACC 4) and two
 CC zucchini (CP-ACC 1A and CP-ACC 1B) ACC synthases.
 CC A novel DNA molecule comprises an expression system which, when
 CC contained in a plant host cell, generates RNA that is sufficiently
 CC complementary to an RNA transcript of an endogenous ACC synthase
 CC gene to prevent its synthesis. The expression system consists of
 CC the reverse transcript of the antisense RNA (i.e. cDNA) operably
 CC linked to control sequences that effect its transcription into the
 CC ACC synthase gene. The cDNA can be amplified from the endogenous
 CC sequences. The DNA molecule can be used to delay ripening of
 CC tomato or zucchini fruits.
 CC
 SQ Sequence 1703 BP; 481 A; 359 C; 378 G; 485 T; 0 other;
 XX
 Query Match 66.1%; Score 15.2; DB 19; Length 1703;
 Best Local Similarity 47.8%; Pred. No. 3.2e+02;
 Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 OY 1 CANANCKRAASMANCCRSYTC 23
 DB 1254 CAACCTCGAACAACCTCGCTC 1232
 XX
 RESULT 13
 AAD04541/C
 ID AAD04541 standard; cDNA: 1703 BP.
 XX
 AC AAD04541;
 XX
 DT 04-JUL-2001 (first entry)
 XX
 DE Zucchini 1-aminocyclopropane-1-carboxylic acid synthase (PACCl) cDNA.
 XX
 KW Zucchini; 1-aminocyclopropane-1-carboxylic acid synthase; PACCl;
 XX ethylene production; fruit ripening; transgenic plant; ss.
 XX
 OS Cucurbita pepo.
 XX
 FH Key Location/Qualifiers
 FT CDS 11..1492
 FT /tag= a
 FT /product= "Zucchini PACCl"
 XX
 XX US6207881-B1.
 PD 27-MAR-2001.
 XX
 PF 25-JAN-1995; 55US-0378313.

XX 19-APR-1992; 92US-0862493.
 PR 10-SEP-1990; 90US-0579896.
 XX
 PA (USDA) US SEC OF AGRIC.
 XX
 PI Theologis A, Sato T;
 XX
 DR WPI: 2001-289591/30.
 DR P-PSDB: AAE00980.
 XX
 PT Novel isolated DNA molecule encoding 1-aminocyclopropane-1-carboxylic
 XX acid synthase, LE-ACC2 useful for producing ACC synthase which is
 XX essential for the production of ethylene in higher plants
 XX
 XX Example 1; Fig 1B; 92pp; English.
 XX
 CC The present sequence is a cDNA encoding zucchini (Cucurbita pepo)
 CC 1-aminocyclopropane-1-carboxylic acid synthase (PACCl). ACC synthase are
 CC capable of catalysing the conversion of Adomet (S-adenosyl methionine)
 CC to ACC and methyl thiodenosine (MTA). ACC DNA is useful for producing
 CC ACC synthase which is essential for the production of ethylene in higher
 CC plants, where ethylene is a determinant of fruit ripening. The ACC DNA
 CC is also useful for producing transgenic plants which are overproducers
 CC of or are deficient in ACC synthase.
 XX
 SQ Sequence 1703 BP; 481 A; 359 C; 378 G; 485 T; 0 other;
 XX
 Query Match 66.1%; Score 15.2; DB 22; Length 1703;
 Best Local Similarity 47.8%; Pred. No. 3.2e+02;
 Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 OY 1 CANANCKRAASMANCCRSYTC 23
 DB 1254 CAACCTCGAACAACCTCGCTC 1232
 XX
 RESULT 14
 AAF23618/C
 ID AAF23618 standard; DNA: 1703 BP.
 XX
 AC AAF23618;
 XX
 DT 22-MAR-2001 (first entry)
 XX
 DE Zucchini ACC synthase clone PACCl coding sequence.
 XX
 KW ACC synthase; 1-aminocyclopropane-1-carboxylic acid synthase;
 XX ethylene production; fruit ripening; enzyme; zucchini; ss.
 XX
 OS Cucurbita pepo.
 XX
 PN US6156956-A.
 XX
 PD 05-DEC-2000.
 XX
 DE 02-MAR-1998; 98US-0033349.
 XX
 PF 25-JAN-1995; 95US-0378313.
 PR 02-APR-1992; 92US-0862493.
 PR 07-JUN-1995; 95US-0481171.
 PR 10-SEP-1990; 90US-0579896.
 XX
 PA (USDA) US DEPT OF AGRICULTURE.
 XX
 PI Sato T, Theologis A;
 XX
 DR WPI: 2001-079558/09.
 DR P-PSDB: AAB59716.
 XX
 PT Expression cassette for producing transgenic plants exhibiting
 XX inhibited ethylene production and delayed fruit ripening, comprises
 XX complementary RNA which inhibits 1-aminocyclopropane-1-carboxylic acid

```

PT synthase synthesis
XX
PS Example 1: Fig 1; 91pp; English.
XX
CC 1-aminocyclopropane-1-carboxylic acid (ACC) synthase is essential for the
CC production of ethylene in higher plants; ethylene is a determinant of
CC fruit ripening. The present invention relates to an expression cassette
CC which comprises the reverse transcript of RNA complementary to an RNA
CC transcribed from ACC synthase gene. The expression cassette can be used
CC to prevent ACC gene expression. The expression cassette is useful for
CC inhibiting ethylene production and fruit ripening, when introduced into a
CC plant or plant cells. The present sequence is the coding sequence for
CC zucchini ACC synthase clone PAC01.
XX
SQ Sequence 1703 BP; 481 A; 359 C; 378 G; 485 T; 0 other;

Query Match      66.1%; Score 15.2; DB 22; Length 1703;
Best Local Similarity 47.8%; Pred. No. 3.2e+02;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 CANANCKRASMAMCNCNRSYTC 23
DB 1254 CAACTCGAACAACCACTGCGCTC 1232
||| 1::1::1||| 1::1::1|||

RESULT 15
AAX27501/C
ID AAX27501 standard; cDNA; 1712 BP.
XX
AC AAX27501:
XX
DT 26-MAY-1999 (first entry)
XX
DE Banana 1-aminocyclopropane-1-carboxylic acid synthase (ACS) cDNA.
XX
KM 1-aminocyclopropane-1-carboxylic acid synthase; ACS; EFE; banana;
KM ethylene forming enzyme; ethylene biosynthesis; plant; fruit ripening;
KM transgenic; enzyme; inhibition; flavour; texture; ss.
XX
OS Musa sp.
XX
PN US5886164-A.
XX
PD 23-MAR-1999.
XX
PE 15-APR-1996; 96US-0632598.
XX
PR 15-APR-1996; 96US-0632598.
XX
PA (ZENEC) ZENECA LTD.
XX
PI Bird CR, Fletcher JD;
XX
DR WPI: 1999-228611/19.
XX
PT Novel isolated cDNA molecules ((PASC6) and (PACOS7)) encoding
PT 1-aminocyclopropane-1-carboxylic acid synthase (ACS) and an ethylene
PT forming enzyme (EFE) - useful for modifying fruit ripening
PT characteristics, especially in bananas
XX
PS Claim 1; Columns 11-14; 22pp; English.
XX
CC The invention relates to two isolated cDNA molecules ((PASC6) and
CC (PACOS7)) encoding 1-aminocyclopropane-1-carboxylic acid synthase (ACS)
CC and an ethylene forming enzyme (EFE), respectively. The clones are
CC deposited under the Accession Numbers NCIMB 40813 and NCIMB 40814,
CC respectively. PASC6 and PACOS7 may be used to genetically control
CC ethylene biosynthesis in plants and hence regulate the ethylene-induced
CC processes involved in fruit ripening (and other ethylene related
CC processes). Vectors comprising the cDNA sequences may be used to produce
CC transgenic bananas with altered fruit ripening characteristics. The
CC orientation of the PASC6 and PACOS7 used in the construct, will determine
CC how the ripening process is affected. If the genes have a sense

```

```

CC orientation, and transcribe mRNA that encodes an active enzyme. The rate
CC of ripening will be increased (up-regulation) (however, full-length sense
CC constructs can also be used to inhibit enzyme expression by co-
CC inhibition). If genes encode antisense mRNA, they will inhibit the
CC expression of the genes involved in fruit ripening and hence slow the
CC process down (down-regulation). In this manner different spatial and
CC temporal patterns of genes expression can be produced. Retardation of the
CC rate of ripening will reduce the rate of deterioration of banana fruit
CC after harvest. This helps in production of high quality fruit that has
CC improved flavour and texture. The present sequence represents the cDNA
CC sequence of the banana ACS enzyme.
XX
SQ Sequence 1712 BP; 397 A; 459 C; 478 G; 378 T; 0 other;

Query Match      66.1%; Score 15.2; DB 20; Length 1712;
Best Local Similarity 47.8%; Pred. No. 3.2e+02;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 CANANCKRASMAMCNCNRSYTC 23
DB 1265 CACACCCCTGACACCCCGCGCTC 1243
||| 1::1::1||| 1::1::1|||

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Job time : 173.5 secs

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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 04:48:25 ; Search time 957.5 Seconds

(without alignments)
699.075 Million cell updates/sec

Title: US-09-975-842-2

Perfect score: 23

Sequence: 1 ggm/ytncngnagtymnrrtng 23

Scoring table:

IDENTITY_NUC
Gapcp:10.0 , Gapext 1.0

Searched: 205640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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8: gb_pl: *
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30: en_vl: *
31: en_vl: *
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33: en_vl: *
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41: en_vl: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.4	67.0	23	AR050170	AR050170 Sequence
2	15.4	67.0	219	TOMACCD	M83329 Lycopersico
3	15.4	67.0	221	LE018058	U18058 Lycopersico
4	15.4	67.0	265	AB005723	AB005723 Actinidia
5	15.4	67.0	265	AF146027	AF146027 Actinidia
6	15.4	67.0	268	AF146026	AF146026 Actinidia
7	15.4	67.0	268	TOMACCA	M83318 Lycopersico
8	15.4	67.0	271	AB005722	AB005722 Actinidia
9	15.4	67.0	271	AF146025	AF146025 Actinidia
10	15.4	67.0	271	TOMACCB	M83320 Lycopersico
11	15.4	67.0	271	TOMACCC	M83322 Lycopersico
12	15.4	67.0	273	PSACS2	X83105 P. sativum m
13	15.4	67.0	308	LEACSLA1	U74450 Lycopersico
14	15.4	67.0	308	LEACSLB1	U74460 Lycopersico
15	15.4	67.0	314	FSY420187	U74461 Lycopersico
16	15.4	67.0	317	AF090351	AJ420187 Fagus syl
17	15.4	67.0	317	AF090351	AF090351 Striga he
18	15.4	67.0	318	FSY420186	AJ420186 Fagus syl
19	15.4	67.0	721	LEU17974	U17974 Lycopersico
20	15.4	67.0	723	AF048753	AF048753 Citrus X
21	15.4	67.0	735	OSACACAS	227242 O. sativa (P
22	15.4	67.0	743	ACU86865	U86865 Actinidia
23	15.4	67.0	757	AF074932	AF074932 Sinapis a
24	15.4	67.0	779	TAU35778	U35778 Trillium ae
25	15.4	67.0	940	AF074931	AF074931 Sinapis a
26	15.4	67.0	941	FSY420188	AJ420188 Fagus syl
27	15.4	67.0	956	AF053355	AF053355 Phaseolus
28	15.4	67.0	960	AF074930	AF074930 Sinapis a
29	15.4	67.0	961	AR135348	AR135348 Sequence
30	15.4	67.0	968	AR135347	AR135347 Sequence
31	15.4	67.0	994	AR093264	AR093264 Sequence
32	15.4	67.0	1008	CSU59813	U59813 Cucumis sat
33	15.4	67.0	1025	CSU59813	U59813 Cucumis sat
34	15.4	67.0	1027	AF074929	AF074929 Sinapis a
35	15.4	67.0	1041	AF074928	AF074928 Sinapis a
36	15.4	67.0	1034	AB015494	AB015494 Passiflor
37	15.4	67.0	1034	AB015495	AB015495 Passiflor
38	15.4	67.0	1080	AF401757	AF401757 Annona ch
39	15.4	67.0	1089	AB021907	AB021907 Musa acum
40	15.4	67.0	1089	AF083815	AF083815 Antirrhin
41	15.4	67.0	1092	CAACCI	X82265 C. annum mRN
42	15.4	67.0	1094	AF083814	AF083814 Antirrhin
43	15.4	67.0	1094	AF518327	AF518327 Populus t
44	15.4	67.0	1094	MDU73815	U73815 Malus domes
45	15.4	67.0	1096	MIU22523	U22523 Mangifera l

ALIGNMENTS

RESULT 1
AR050170
LOCUS AR050170 23 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5824875.
ACCESSION AR050170
VERSION AR050170.1 GI:5972162
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Kenu, R.S.
TITLE 1-aminocyclopropane-1-carboxylate synthase genes from pelargonium
JOURNAL Patent: US 5824875-A 9 20-Oct-1998;
FEATURES Location/Qualifiers

source	1. .23	/organism="unknown"
BASE COUNT	0 a 2 c 7 g 4 t 10 others	
ORIGIN		
Query Match	67.0%;	Score 15.4; DB 6; Length 23;
Best Local Similarity	100.0%;	Pred. No. 2.1e+03;
Matches 23; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY	1	GGNYTNCNGGNTTYMGRTNGG 23
Db	1	GGNYTNCNGGNTTYMGRTNGG 23
RESULT 2		
TOMACCD		219 bp mRNA linear PLN 19-JUN-1995
LOCUS		
DEFINITION		Lycopersicon esculentum 1-aminocyclopropane-1-carboxylate homologue
ACCESSION		M83329
VERSION		M83329.1 GI:170510
KEYWORDS		1-aminocyclopropane-1-carboxylate synthase; homologue.
SOURCE		Lycopersicon esculentum ripe pericarp CDNA to mRNA.
ORGANISM		Lycopersicon esculentum
REFERENCE		Eukaryota: Viridiplantae; Streptophyta: Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; easterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
AUTHORS		1 (bases 1 to 219)
TITLE		Yip,W.K., Moore,T. and Yang,S.F.
JOURNAL		Differential accumulation of transcripts for four tomato
MEDLINE		1-aminocyclopropane-1-carboxylate synthase under various
PUBMED		conditions
FEATURES		Proc. Natl. Acad. Sci. U.S.A. 89 (6), 2475-2479 (1992)
source		1549612
	Location/Qualifiers	
	1. .219	
	/organism="Lycopersicon esculentum"	
	/db_xref="taxon:4081"	
	/rlnsue_type="pericarp"	
	/dev_stage="ripe"	
	<1. .>219	
	/EC_number="4.4.1.14"	
	/note="homologue"	
	/codon_start=1	
	/product="1-aminocyclopropane-1-carboxylate synthase"	
	/protein_id="AAA68623.1"	
	/db_xref="GI:867993"	
	/translation="EHNHILVCDELYATVPNPPKFSVIAEINEDNCINKDLVHVS	
	SLSKDLGPFGRGIVGISEFNDVYVCAK"	
BASE COUNT	67 a 38 c 41 g 73 t	
ORIGIN		
Query Match	67.0%;	Score 15.4; DB 8; Length 219;
Best Local Similarity	56.5%;	Pred. No. 1.1e+03;
Matches 13; Conservative	4; Mismatches 6; Indels 0; Gaps 0;	
OY	1	GGNYTNCNGGNTTYMGRTNGG 23
Db	151	GGTTCACAGATTCGAGTGG 173
RESULT 3		
LOCUS		LEU18058 221 bp DNA linear PLN 08-MAR-1997
DEFINITION		Lycopersicon esculentum 1-aminocyclopropane-1-carboxylate synthase
ACCESSION		(LE-ACS5) DNA, partial cds.
VERSION		U18058
KEYWORDS		U18058.1 GI:1561701
SOURCE		Lycopersicon esculentum.
ORGANISM		Lycopersicon esculentum

REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE	Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
JOURNAL	Lycopersicon.
REFERENCE	1 (bases 1 to 221)
AUTHORS	Krawakita,K., Hennig,L., Lincoln,J.E., Rottmann,W.H., Campbell,A.D.,
TITLE	Zarembinski,T.J., Yu,G.X., Taylor,L.D. and Theologis,A.
JOURNAL	The tomato l-aminocyclopropane-1-carboxylate (ACC) synthase
	multigenic family is encoded by at least eight members
	Unpublished
	2 (bases 1 to 221)
	Direct Submission
	Submitted (01-DEC-1994) Athanasios Theologis, Plant Gene Expression
	Center, ARS/USDA, 800 Buchanan Street, Albany, CA 94710 and
	Department of Plant Biology, University of California, Berkeley, CA
	94720, USA
FEATURES	
SOURCE	Location/Qualifiers
	1..221
	/organism="Lycopersicon esculentum"
	/cultivar="Rutgers"
	/db_xref="taxon:4081"
	/clone="PSEF3 (stock #394)"
	1..221
gene	/gene="LE-ACS5"
	<1..>221
CDS	/gene="LE-ACS5"
	/EC_number="4.4.1.14"
	/function="converts SAM to ACC; plant hormone
	biosynthesis"
	/standard_name="Lycopersicon esculentum l-amino-
	cyclopropane-1-carboxylate synthase"
	/note="direct precursor of ethylene; one member of a
	multigenic family; from TZ region to the reaction center;
	similar to the product encoded by PIR Accession Number
	C41985"
	/codon_start=1
	/product="ACC synthase"
	/protein_id="AAB48947.1"
	/db_xref="GI:1561702"
	/translation="TLITFMFKIHIVSDPEIACGYFDSPKFEVSIETALDRLEKRS
	KMNQVHIVSLSSLDLGPRGVGMITSN"
BASE COUNT	79 a 41 c 40 g 61 t -
ORIGIN	
Query Match	67.0%; Score 15.4; DB 8; Length 221;
Best Local Similarity	56.5%; Pred. No. 1.6e+03;
Matches 13; Conservative	4; Mismatches 6; Indels 0; Gaps 0;
QY	1 GGNATNCNGGNTWTMGNTTNGC 23
	: ::
DB	181 GGCGTTCCAGGTTTCAGACTTG 203
RESULT 4	
LOCUS	AB005723 265 bp mRNA linear PLN 22-JUL-1997
DEFINITION	Actinidia deliciosa mRNA for ACC synthase, partial cds.
ACCESSION	AB005723
VERSION	AB005723.1 GI:2274792
KEYWORDS	ACC synthase.
SOURCE	Actinidia deliciosa (sub_species:deliciosa, strain:Hayward)
	wound-treated fruit cdna to mRNA.
ORGANISM	Actinidia deliciosa
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
	Asteridae; Ericales; Actinidiaceae; Actinidia.
REFERENCE	1 (sites)
AUTHORS	Ikoma,Y., Yano,M. and Ogawa,K.
TITLE	Cloning and expression of genes encoding ACC synthase in kiwifruit
JOURNAL	Acta Horticulturae 398, 179-186 (1995)
REFERENCE	2 (bases 1 to 265)
AUTHORS	Ikoma,Y.

Matches	13:	Conservative	4:	Mismatches	6:	Indels	0:	Gaps	0:
QY	1	GCNTNCCNGGNTTYMGNTNGC	23						
Db	198	GGCTCCCGGGTTCAGGCTCG	220						
RESULT 6									
AF146026			268 bp	DNA		linear	PLN 17-MAY-1999		
LOCUS		Actinidia chinensis 1-aminocyclopropane-1-carboxylate synthase 1B							
DEFINITION		gene, partial cds.							
ACCESSION		AF146026							
VERSION		AF146026.1		GI:4836798					
KEYWORDS									
SOURCE		Actinidia chinensis.							
ORGANISM		Actinidia chinensis							
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Actinidiaceae; Actinidia.							
AUTHORS		1 (bases 1 to 268)							
TITLE		Xu,C., Chen,K., Chen,D. and Zhang,S. ACC synthase gene family from kiwifruit (Actinidia chinensis Planch.) unpublished							
JOURNAL		2 (bases 1 to 268)							
REFERENCE		Xu,C., Chen,D., Chen,K. and Zhang,S.							
AUTHORS		Direct Submission							
TITLE		Submitted (27-APR-1999) Department of Horticulture, Huajiachi Campus, Zhejiang University, Kaixuanlu 268, Hangzhou, Zhejiang 310029, People's Republic of China							
JOURNAL		Location/Qualifiers							
FEATURES		1..268							
SOURCE		/organism="Actinidia chinensis"							
		/db_xref="taxon:3625"							
		<1..>268							
		/note="Actinidia chinensis Planch"							
		/note="ACSB"							
		/codon_start=3							
		/product="1-aminocyclopropane-1-carboxylate synthase 1B"							
		/protein_id="AAD30561.1"							
		/db_xref="GI:4836799"							
		/translation="TLRPELNLILFRITSKNILHLSDEITVSGTVPSSPFSYIMEVILKSSHTEVMKRVHIVSLSKDGLPEFGFAGALYSMDVVAAT"							
BASE COUNT		63 a	82 c	58 g	65 t				
ORIGIN									
Query Match		67.0%;	Score 15.4;	DB 8;	Length 268;				
Best Local Similarity		56.5%;	Pred. NO. 1.6e+03;						
Matches 13;		Conservative	4;	Mismatches	6;	Indels	0;	Gaps	0;
QY	1	GGNTNCCNGGNTTYMGNTNGC	23						
Db	204	GGTCTCCCGGGTTCGCGGCTCG	226						
RESULT 7									
TOMACCA			268 bp	mRNA		linear	PLN 19-JUN-1995		
LOCUS		TOMACCA							
DEFINITION		Tomopsericon esculentum 1-aminocyclopropane-1-carboxylate homologue mRNA, partial cds.							
ACCESSION		MR83318							
VERSION		MR83318.1		GI:170505					
KEYWORDS		1-aminocyclopropane-1-carboxylate synthase; homologue.							
SOURCE		Tomopsericon esculentum red ripe fruit pericarp cDNA to mRNA.							
ORGANISM		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;							
REFERENCE		1 (bases 1 to 268)							
AUTHORS		Yip,W.K., Moore,T. and Yang,S.F.							
TITLE		Differential accumulation of transcripts for four tomato							

1-aminocyclopropane-1-carboxylate synthase homologs under various conditions
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (6), 2475-2479 (1992)
 MEDLINE 92196141
 PUBMED 1549612

FEATURES
 source Location/Qualifiers
 1..268

/organism="Lycopersicon esculentum"
 /db_xref="taxon:4081"
 /tissue_type="pericarp"
 /dev_stage="red ripe fruit"
 <1..>268
 /EC_number="4.4.1.14"
 /note="homologue"

/codon_start=2
 /product="1-aminocyclopropane-1-carboxylate synthase"
 /protein_id="AA68621.1"

/db_xref="GI:867990"

/translation="LDKDTLRSVLSFNNQNHILVCEIYATVPDPQVSIETILD
 EDEMTCMKDLVHIVYSLSKDMLGPFGRVGIYSFNDVVNCARK"

BASE COUNT 86 a 58 c 49 g 75 t

ORIGIN

Query Match 67.0%; Score 15.4; DB 8; Length 268;
 Best Local Similarity 56.5%; Pred. No. 1.6e+03;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNATCCGNGNTYMGNTNG 23

DB 300 GGGTTACGAGATTAGAGTCG 222

RESULT 8
 LOCUS AB005722 271 bp mRNA linear PLN 22-JUL-1997
 DEFINITION Actinidia deliciosa mRNA for ACC synthase, partial cds.
 ACCESSION AB005722.1 GI:2275789
 KEYWORDS ACC synthase.
 SOURCE Actinidia deliciosa (subspecies:deliciosa, strain:Hayward)
 ethylene-treated fruit cDNA to mRNA.

ORGANISM Actinidia deliciosa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; Ericales; Actinidiaceae; Actinidia.

REFERENCE 1 (sites)
 Ikoma,Y., Yano,M. and Ogawa,K.

AUTHORS Cloning and expression of genes encoding ACC synthase in kiwifruit
 TITLE Acta Horticulture 398, 179-186 (1995)

JOURNAL 2 (bases 1 to 271)
 REFERENCE Ikoma,Y.

TITLE Direct Submission
 JOURNAL Submitted (11-JUL-1997) Yoshinori Ikoma, National Institute of
 Fruit Tree Science, Department of Citriculture; Okitsu, Shimizu,
 Shizuoka 424-02, Japan (E-mail:yoshinok@ok.affrc.go.jp,
 Tel:+81-543-69-7111, Fax:+81-543-69-2115)

FEATURES
 source Location/Qualifiers
 1..271

/organism="Actinidia deliciosa"
 /strain="Hayward"
 /sub_species="deliciosa"
 /db_xref="taxon:3627"
 /tissue_type="ethylene-treated fruit"
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 /codon_start=2
 /product="ACC synthase"
 /protein_id="BA21557.1"
 /db_xref="GI:2275790"

CDS

/translation="TLTRPELNLTLFITSKNHILISDEIYSGTVFSSPFWISMEFL
 KDSHSTFVNRVHIVYSLSKDGLGPFGRVGAIYSNDVVLAARK"

BASE COUNT 67 a 82 c 56 g 66 t

ORIGIN

Query Match 67.0%; Score 15.4; DB 8; Length 271;
 Best Local Similarity 56.5%; Pred. No. 1.6e+03;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNATCCGNGNTYMGNTNG 23

DB 203 GGTCTCCGCGGTTCCGGTCG 225

RESULT 9

LOCUS AF146025 271 bp DNA linear PLN 17-MAY-1999

DEFINITION Actinidia chinensis 1-aminocyclopropane-1-carboxylate synthase 1A

ACCESSION AF146025

VERSION AF146025.1 GI:4836796

KEYWORDS

SOURCE

ORGANISM

Actinidia chinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; Ericales; Actinidiaceae; Actinidia.

REFERENCE 1 (bases 1 to 271)
 Xu,C., Chen,K., Chen,D. and Zhang,S.

AUTHORS Molecular cloning of four members of ACC synthase gene family from
 kiwifruit (Actinidia chinensis Planch.)
 TITLE Unpublished

JOURNAL 2 (bases 1 to 271)
 REFERENCE Xu,C., Chen,D., Chen,K. and Zhang,S.

AUTHORS Direct Submission
 TITLE Submitted (27-APR-1999) Department of Horticulture, Huajiach
 Campus, Zhejiang University, Kaixuanlu 268, Hangzhou, Zhejiang
 310029, People's Republic of China

JOURNAL Location/Qualifiers
 1..271

/organism="Actinidia chinensis"
 /db_xref="taxon:3625"
 /note="Actinidia chinensis Planch"

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 /note="ACSLA"
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 /protein_id="AB030860.1"
 /db_xref="GI:4836797"

/translation="TLTRPELNLTLFITSKNHILISDEIYSGTVFSSPFWISMEVL
 KDSHSTFVNRVHIVYSLSKDGLGPFGRVGAIYSNDVVVAAS"

BASE COUNT 67 a 84 c 55 g 65 t

ORIGIN

Query Match 67.0%; Score 15.4; DB 8; Length 271;
 Best Local Similarity 56.5%; Pred. No. 1.6e+03;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNATCCGNGNTYMGNTNG 23

DB 204 GGTCTCCGCGGTTCCGGTCG 226

RESULT 10
 LOCUS TOMACCB 271 bp mRNA linear PLN 19-JUN-1995
 DEFINITION Lycopersicon esculentum 1-aminocyclopropane-carboxylate synthase
 homologous mRNA, partial cds.
 ACCESSION M83320.1 GI:170508
 VERSION M83320

KEYWORDS

SOURCE

ORGANISM

Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

REFERENCE Lycopersicon,
 1 (bases 1 to 271)

AUTHORS		Vid.M.K., Moore,T. and Yang,S.F.	
TITLE		Differential accumulation of transcripts for four tomato 1-aminocyclopropane-1-carboxylate synthase homologs under various conditions	
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 89 (6), 2475-2479 (1992)	
MEDLINE		9219614	
PUBMED		1549612	
FEATURES		source	
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		/note="homologue"	
		/codon_start=2	
		/product="1-aminocyclopropane-1-carboxylate synthase"	
		/protein_id="AAA68622.1"	
		/db_xref="GI:867991"	
		/translation="LMRNLELLTFPEKGIHLISDEISGTVPNSPGFVSMEVLI	
		EKMYTRVENVHIVYSKIDLGPGFRIGATYSNDENVSAATK"	
BASE COUNT		78 a 62 c 55 g 76 t	
ORIGIN			
Query Match		67.0%; Score 15.4; DB 8; Length 271;	
Best Local Similarity		56.5%; Pred. No. 1.6e+03;	
Matches 13; Conservative		4; Mismatches 6; Indels 0; Gaps 0;	
OY		1 GGNATNCNGNTTYMGNRTNG 23	
Db		203 GGCTCCCGGTTTCCCATTTGG 225	
RESULT 11			
LOCUS		271 bp mRNA linear PLN 30-JUN-1997	
DEFINITION		Lycopersicon esculentum 1-aminocyclopropane-carboxylate synthase	
ACCESSION		M83322	
VERSION		M83322.1	
KEYWORDS		GI:295351	
SOURCE		Lycopersicon esculentum.	
ORGANISM		Lycopersicon esculentum.	
REFERENCE		Bakayorta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; easterids I; Solanales; Solanaceae; Solanum; Lycopersicon.	
AUTHORS		1 (bases 1 to 271)	
TITLE		Vid.M.K., Moore,T. and Yang,S.F.	
		Differential accumulation of transcripts for four tomato 1-aminocyclopropane-1-carboxylate synthase homologs under various conditions	
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 89 (6), 2475-2479 (1992)	
MEDLINE		9219614	
PUBMED		1549612	
FEATURES		source	
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		/organism="Lycopersicon esculentum"	
		/db_xref="taxon:4081"	
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		<1. >271	
		/EC_number="4.4.1.14"	
		/note="homologue"	
		/codon_start=2	
		/product="1-aminocyclopropane-1-carboxylate synthase"	
		/protein_id="AAA68622.1"	
		/db_xref="GI:867991"	
		/translation="LMRNLELLTFPEKGIHLISDEISGTVPNSPGFVSMEVLI	
		EKMYTRVENVHIVYSKIDLGPGFRIGATYSNDENVSAATK"	
BASE COUNT		78 a 62 c 55 g 76 t	
ORIGIN			
Query Match		67.0%; Score 15.4; DB 8; Length 271;	
Best Local Similarity		56.5%; Pred. No. 1.6e+03;	
Matches 13; Conservative		4; Mismatches 6; Indels 0; Gaps 0;	
OY		1 GGNATNCNGNTTYMGNRTNG 23	
Db		203 GGCTCCCGGTTTCCCATTTGG 225	
RESULT 12			
LOCUS		273 bp mRNA linear PLN 09-OCT-1995	
DEFINITION		Pisum sativum mRNA for 1-aminocyclopropane-1-carboxylate synthase (partial).	
ACCESSION		X83105.1	
VERSION		X83105.1	
KEYWORDS		GI:602079	
SOURCE		1-aminocyclopropane-1-carboxylate synthase; acs2 gene.	
ORGANISM		Pisum sativum.	
REFERENCE		Bakayorta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eusterids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.	
AUTHORS		1 (bases 1 to 273)	
TITLE		Beck,S.C. and Kende,H.	
JOURNAL		Sequential induction of the ethylene biosynthetic enzymes by indole-3-acetic acid in etiolated peas	
MEDLINE		95322591	
PUBMED		7599314	
FEATURES		source	
		.273	
		/organism="Pisum sativum"	
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		/tissue-type="calyx"	
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		/EC_number="4.4.1.14"	
		/note="homologue"	
		/codon_start=1	
		/product="1-aminocyclopropane-1-carboxylate synthase"	
		/protein_id="CAA58167.1"	
		/db_xref="GI:602080"	
		/translation="TYMDNRTLVTFITNEKRHLISDEIYATVTSHPFSIAET	
		IENDYDIEDRNLVHIVYSKIDLGPGFRIGATYSNDYVDCTRK"	
BASE COUNT		90 a 61 c 52 g 70 t	
ORIGIN			
Query Match		67.0%; Score 15.4; DB 8; Length 273;	
Best Local Similarity		56.5%; Pred. No. 1.6e+03;	
Matches 13; Conservative		4; Mismatches 6; Indels 0; Gaps 0;	
OY		1 GGNATNCNGNTTYMGNRTNG 23	
Db		205 GGATTCGGGGGTATGAGTTGG 227	

RESULT 13
LEAC51A1
LOCUS 308 bp DNA linear PLN 16-APR-1997
DEFINITION Lycopersicon esculentum 1-aminocyclopropane-1-carboxylate synthase (LE-ACS1A) gene, partial cds.
ACCESSION U74458.1 GI:1814255
VERSION 1
KEYWORDS 1 of 2
SEGMENT Lycopersicon esculentum.
SOURCE Lycopersicon esculentum.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 308)
AUTHORS Oetliker, J.H., Olson, D.C., Shiu, O.Y. and Yang, S.F.
TITLE Differential induction of seven 1-aminocyclopropane-1-carboxylate synthase genes by elicitor in suspension cultures of tomato (Lycopersicon esculentum)
JOURNAL Plant Mol. Biol. 34 (2), 275-286 (1997)
MEDLINE 9207843
PUBMED 9207843
AUTHORS Oetliker, J.H., Olson, D.C., Shiu, O.Y. and Yang, S.F.
TITLE Direct Submission
JOURNAL Submitted (25-SEP-1996) Vegetable Crops, University of California at Davis, Mann Laboratory, Davis, CA 95616, USA
FEATURES
source 1..308
/organism="Lycopersicon esculentum"
/db_xref="taxon:4081"
CDS
/gene="LE-ACS1A"
/EC_number="4.4.1.14"
/note="active site region; stop codon immediately upstream of CDS is an artifact from the PCR primer sequence"
/codon_start=1
/product="1-aminocyclopropane-1-carboxylate synthase"
/protein_id="AAC49689.1"
/db_xref="GI:1814258"
/translation="NPLGTLDDKDLTLDIVTFINSKNHIVCDEIYAATVDPREIS VSEIWEEMIECNLDLHIVYSLSKDLGFPEFRVGIYSTNDTVNIAKRMSSFGLV"
BASE COUNT 95 a 55 c 63 g 95 t
ORIGIN
Query Match 67.0%; Score 15.4; DB 8; Length 308;
Best Local Similarity 56.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 GGNVTCNCNGNTTYMGNTNGG 23
Db 220 GGATTTCCAGATTCAGAGTTGG 242
RESULT 14
LEAC51B1
LOCUS 308 bp mRNA linear PLN 16-APR-1997
DEFINITION Lycopersicon esculentum 1-aminocyclopropane-1-carboxylate synthase (LE-ACS1B) mRNA, partial cds.
ACCESSION U74460
VERSION 1
KEYWORDS 1 of 2
SEGMENT Lycopersicon esculentum.
SOURCE Lycopersicon esculentum.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 308)
AUTHORS Oetliker, J.H., Olson, D.C., Shiu, O.Y. and Yang, S.F.
TITLE Differential induction of seven 1-aminocyclopropane-1-carboxylate

synthase genes by elicitor in suspension cultures of tomato (Lycopersicon esculentum)
JOURNAL Plant Mol. Biol. 34 (2), 275-286 (1997)
MEDLINE 9207843
PUBMED 9207843
AUTHORS Oetliker, J.H., Olson, D.C., Shiu, O.Y. and Yang, S.F.
TITLE Direct Submission
JOURNAL Submitted (25-SEP-1996) Vegetable Crops, University of California at Davis, Mann Laboratory, Davis, CA 95616, USA
FEATURES
source 1..308
/organism="Lycopersicon esculentum"
/db_xref="taxon:4081"
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/note="active site region"
/codon_start=1
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/protein_id="AAC49683.1"
/db_xref="GI:1814264"
/translation="NPSNPLGTLDDKDLTLDIVTFINSKNHIVCDEIYAATVDPREIS VSEIWEEMIECNLDLHIVYSLSKDLGFPEFRVGIYSTNDTVNIAKRMSSFGLV"
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ORIGIN
Query Match 67.0%; Score 15.4; DB 8; Length 308;
Best Local Similarity 56.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 GGNVTCNCNGNTTYMGNTNGG 23
Db 220 GGATTTCCAGATTCAGAGTTGG 242
RESULT 15
LEAC56
LOCUS 308 bp mRNA linear PLN 16-APR-1997
DEFINITION Lycopersicon esculentum 1-aminocyclopropane-1-carboxylate synthase (LE-ACS6) mRNA, partial cds.
ACCESSION U74461
VERSION 1
KEYWORDS 1 of 2
SEGMENT Lycopersicon esculentum.
SOURCE Lycopersicon esculentum.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 308)
AUTHORS Oetliker, J.H., Olson, D.C., Shiu, O.Y. and Yang, S.F.
TITLE Differential induction of seven 1-aminocyclopropane-1-carboxylate synthase genes by elicitor in suspension cultures of tomato (Lycopersicon esculentum)
JOURNAL Plant Mol. Biol. 34 (2), 275-286 (1997)
MEDLINE 9207843
PUBMED 9207843
AUTHORS Oetliker, J.H., Olson, D.C., Shiu, O.Y. and Yang, S.F.
TITLE Direct Submission
JOURNAL Submitted (25-SEP-1996) Vegetable Crops, University of California at Davis, Mann Laboratory, Davis, CA 95616, USA
FEATURES
source 1..308
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/db_xref="taxon:4081"
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BASE COUNT 94 a 58 c 62 g 94 t
ORIGIN

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/gene="LE-AC56"
/EC-number="4.4.1.14"
/note="stop codon immediately upstream of CDS is an
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/codon-start=1
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/db_xref="GI:1814265"
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ISEKSVSCNDLDLHVIVSLSDLPFGFRGILSYNDAAVNIAKRMSSFLY"
BASE COUNT      98 a
ORIGIN            53 c      63 g      94 t
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Query Match	67.08;	Score 15.4;	DB 8;	Length 308;
Best Local Similarity	56.58;	Pred. No. 1.6e+03;		
Matches 13; Conservative	4;	Mismatches 6;	Indels 0;	Gaps 0;

Qy	1	GGNYTNCNGSNITYMGNRTNGG	23
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Db	220	GGGTTCCCTGSAITTAGGGTTGG	242

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GenCore version 5.1.4-p5-4578
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 04:48:25 ; Search time 957.5 seconds
(without alignments)

699.075 Million cell updates/sec

Title: US-09-975-842-3

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Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database :

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2: gb_hg: *
3: gb_in: *
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14: gb_vl: *
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18: gb_om: *
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32: gb_om: *
33: gb_ov: *
34: gb_ph: *
35: gb_pl: *
36: gb_pr: *
37: gb_ro: *
38: gb_sts: *
39: gb_sy: *
40: gb_un: *
41: gb_vi: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.2	66.1	23	6 AR050171	AR050171 Sequence
2	15.2	66.1	621	8 MS087152	U87152 Musa acumin
3	15.2	66.1	697	8 AF049138	AF049138 Dianthus
4	15.2	66.1	894	8 AF184076	AF184076 Prunus ar
5	15.2	66.1	1089	8 AY061946	AY061946 Rosa hybr
6	15.2	66.1	1089	8 CAA001	C82265 C. annuum mRN
7	15.2	66.1	1094	8 MDU73815	MDU73815 Malus domes
8	15.2	66.1	1096	8 MIU02523	MIU02523 Mangifera l
9	15.2	66.1	1097	8 AF467782	AF467782 Prunus pe
10	15.2	66.1	1098	8 ARU79524	ARU79524 Arabidopsi
11	15.2	66.1	1098	8 STU70842	STU70842 Solanum tub
12	15.2	66.1	1100	8 AF239989	AF239989 Prunus pe
13	15.2	66.1	1100	8 CPA01257	CPA01257 Carica pa
14	15.2	66.1	1100	8 AF120898	AF120898 Carica pa
15	15.2	66.1	1101	8 AF184076	AF184076 Prunus ar
16	15.2	66.1	1104	8 VRACCSYN	VRACCSYN Prunus ar
17	15.2	66.1	1106	8 AF120899	AF120899 Betula pe
18	15.2	66.1	1109	8 AF338652	AF338652 Brassica
19	15.2	66.1	1110	8 D37937	D37937 Cucumis mel
20	15.2	66.1	1113	8 D86241	D86241 Cucumis mel
21	15.2	66.1	1113	8 AF144746	AF144746 Solanum m
22	15.2	66.1	1123	8 AF184077	AF184077 Prunus ar
23	15.2	66.1	1164	8 PHU17231	PHU17231 Pelargonium
24	15.2	66.1	1170	8 AF178077	AF178077 Carica pa
25	15.2	66.1	1192	8 AF178076	AF178076 Carica pa
26	15.2	66.1	1194	8 AF177769	AF177769 Carica pa
27	15.2	66.1	1206	8 AF239663	AF239663 Prunus pe
28	15.2	66.1	1320	8 VRACCSYN4	VRACCSYN4 Prunus pe
29	15.2	66.1	1340	8 AF332390	AF332390 Arabidops
30	15.2	66.1	1344	8 AF222638	AF222638 Influenza
31	15.2	66.1	1362	14 MSBACS20E	MSBACS20E Musa acumin
32	15.2	66.1	1372	8 AF332405	AF332405 Arabidops
33	15.2	66.1	1383	8 VRACCSYN5	VRACCSYN5 Vigna radi
34	15.2	66.1	1393	8 VRACCSYN5	VRACCSYN5 Vigna radi
35	15.2	66.1	1393	8 CPA277160	CPA277160 Carica pa
36	15.2	66.1	1394	8 AF312737	AF312737 Malus x d
37	15.2	66.1	1400	8 AF334712	AF334712 Arabidops
38	15.2	66.1	1410	8 LEU17972	LEU17972 Lycopersico
39	15.2	66.1	1413	8 AF334720	AF334720 Arabidops
40	15.2	66.1	1413	8 AF334720	AF334720 Arabidops
41	15.2	66.1	1413	8 AF334720	AF334720 Arabidops
42	15.2	66.1	1425	8 AF332404	AF332404 Arabidops
43	15.2	66.1	1425	8 AF332404	AF332404 Arabidops
44	15.2	66.1	1425	8 AF332404	AF332404 Arabidops
45	15.2	66.1	1433	8 CPA277161	CPA277161 Carica pa

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
AR050171	AR050171	Sequence 10 from patent US 5824875.	AR050171	AR050171.1	GI:5972163	Unknown.	Unknown.	1 (bases 1 to 23)	Ranu, R.S.	1-aminocyclopropane-1-carboxylate synthase genes from pelargonium	Patent: US 5824875-A 10 20-OCT-1998;	Location/Qualifiers

source 1. 23
/organism="unknown"

BASE COUNT 5 a 5 c 0 g 1 t 12 others

ORIGIN

Query Match 66.1%; Score 15.2; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CANANCKRASMNCNRSYTC 23
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Db 1 CANANCKRASMNCNRSYTC 23
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RESULT 2
MS087152/c 621 bp mRNA linear PLN 18-FEB-1997
LOCUS
DEFINITION Musa acuminata 1-aminocyclopropane-1-carboxylate synthase (BACS4)
ACCESSION U87152
VERSION U87152.1 GI:1842048
KEYWORDS
SOURCE Musa acuminata.
ORGANISM Musa acuminata.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
Musa.
REFERENCE 1 (bases 1 to 621)
AUTHORS Pua, E.-C. and Liu, J.-J.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-1997) Department of Biological Sciences, Michigan
Technological University, Houghton, MI 49931, USA
location/Qualifiers

FEATURES
source 1. 621
/organism="Musa acuminata"
/strain="AAA group, cavendish"
/db_xref="taxon:4641"
1. 621
/gene="BACS4"
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/protein_id="AAB47554.1"
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BASE COUNT 120 a 169 c 199 g 133 t

ORIGIN

Query Match 66.1%; Score 15.2; DB 8; Length 621;
Best Local Similarity 47.8%; Pred. No. 1.5e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 CANANCKRASMNCNRSYTC 23
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Db 608 CAGACCGGACACCCCGGCTC 586
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RESULT 3
AF049138/c 697 bp mRNA linear PLN 11-MAR-1998
LOCUS
DEFINITION Dianthus caryophyllus 1-aminocyclopropane-1-carboxylate synthase 2
(ACS2) mRNA, partial cds.
ACCESSION AF049138
VERSION AF049138.1 GI:2947285
KEYWORDS
SOURCE Dianthus caryophyllus.
ORGANISM Dianthus caryophyllus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Caryophyllaceae; Dianthus.
REFERENCE 1 (bases 1 to 697)
AUTHORS Jones, M.L., Larsen, P.B. and Woodson, W.R.
TITLE Differential expression of three members of the ACC synthase gene
family in carnation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 697)
AUTHORS Jones, M.L., Larsen, P.B. and Woodson, W.R.
TITLE Direct Submission
JOURNAL Submitted (17-FEB-1998) Horticulture and Landscape Architecture,
Purdue University, 1165 Horticulture, West Lafayette, IN
47907-1165, USA
location/Qualifiers

FEATURES
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/organism="Dianthus caryophyllus"
/cultivar="white sin"
/db_xref="taxon:3570"
<1..697
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/note="similar to protein encoded by GenBank Accession
Number X66605"
/codon_start=3
/product="1-aminocyclopropane-1-carboxylate synthase 2"
/protein_id="AAC05377.1"
/db_xref="GI:2947286"
/translation="KRLPTKRLGLGSLGVGQTLKSSVGLFVWMDLRHMDPTVE
GELIMRWIINPKVKNIPSSSPCHPCPEPFPCINMNDMEVALRTRFEVLRIR
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BASE COUNT 205 a 119 c 166 g 207 t

ORIGIN

Query Match 66.1%; Score 15.2; DB 8; Length 697;
Best Local Similarity 47.8%; Pred. No. 1.5e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 CANANCKRASMNCNRSYTC 23
|||||

Db 235 CAGACTCTGACACCCGCGCTC 213
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RESULT 4
AF184076/c 894 bp DNA linear PLN 01-OCT-2000
LOCUS
DEFINITION Prunus armeniaca ACC synthase (ACS1) gene, partial cds.
ACCESSION AF184076
VERSION AF184076.1 GI:10441264
KEYWORDS
SOURCE Prunus armeniaca.
ORGANISM Prunus armeniaca.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
REFERENCE 1 (bases 1 to 894)
AUTHORS Mbeugue-A-Mbeugue, D. and Fils-Lycaon, B.R.
TITLE Molecular cloning and nucleotide sequence of genomic DNA encoding
ACC synthase from apricot fruit
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 894)
AUTHORS Mbeugue-A-Mbeugue, D. and Fils-Lycaon, B.R.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-1999) Station de Technologie des Produits
Vegetaux, Institut National de la Recherche Agronomique,
Agroparc-Domaine Saint Paul, Avignon 84914, France
location/Qualifiers

FEATURES
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/organism="Prunus armeniaca"
/db_xref="taxon:36596"
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/gene="ACS1"

[illegible][illegible]

SOURCE	Malus x domestica.
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids I; Rosales; Rosaceae; Maloideae; Malus.
REFERENCE AUTHORS TITLE	1 (bases 1 to 1094) Rosentfield,C.-L., Kiss,E. and Hrazdina,G. MADS-2 (Accession No. U73815) and MdACS-3(Accession No. U73816): two new l-aminocyclopropane-1-carboxylate synthases in ripening apple fruit (PCR95-122)
JOURNAL REFERENCE AUTHORS TITLE	Plant Physiol. 112, 1735 (1996) 2 (bases 1 to 1094) Rosentfield,C.-L., Kiss,E. and Hrazdina,G. Direct Submission Submitted (09-OCT-1996) Food Science & Technology, Cornell University, NYSAES, Geneva, NY 14456, USA
FEATURES	Location/Qualifiers
SOURCE	1..1094 /organism="Malus x domestica" /strain="McIntosh" /db_xref="taxon:3750" /tissue_type="ripening apple fruit"
gene	1..1094 /gene="MdACS-2"
CDS	<1..>1094 /gene="MdACS-2" /EC_number="4.1.1.14" /codon_start=1 /product="ACC synthase" /protein_id="AAB67988.1" /db_xref="GI:1658060" /translation="QMGLAEHQPCFDLLIQEMVNNPKASICTYEGVDPEDDIAIFQDYHGLEPFRKAVARFMEKRGDVRVFDPRIWMSGATGAHSLEAFCLADPEDAVLPFYPEPDFRLRWRTVOQLPPVVCSSNFKRYTKALEAKYKAQESNIKYGLIINNSNPICITLDKETLKDLRFINDKNHLVCEDEIVATALCOFSFISISEVMNEVGCDNLVHVYSIKSDIGPFGRVGIIYINYNVNVIARKMSFGSVSTOTRILIASMLSDTI FVENPIKSAMKLRSORHDLPFKGGOVEITTLKSNAGLFLIMDLRRFTENSTFDEELK LWHIIIRNVKLINSFGCSFHCSPEGMWRVC"
BASE COUNT	357 a 171 c 229 g 337 t
ORIGIN	
Query Match	66.1%; Score 15.2; DB 8; Length 1094;
Best Local Similarity	47.8%; Pred. No. 1.4e+03;
Matches	11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
Oy	1 CANANNCKRASMANCCNRSYTC 23 :: :: :: :: Db 1091 CATACCCGGAGCAACTGTGCCTC 1069
RESULT 8	
MU022523/c	1096 bp mRNA linear PLN 01-JAN-1996
LOCUS	
DEFINITION	Mangifera indica l-aminocyclopropane-carboxylate synthase mRNA, partial cds.
ACCESSION	U22523
VERSION	U22523.1 GI:1143811
KEYWORDS	
SOURCE	
ORGANISM	Mangifera indica.
REFERENCE	Mangifera indica
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Sapindales; Anacardiaceae; Mangifera.
TITLE	1 (bases 1 to 1096) Botella,J.R. Ethylene evolution and ACC synthase gene expression during ripening of mango fruits
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1096) Botella,J R. Direct Submssion
AUTHORS	Submitted (14-MAR-1995) Jose R. Botella, Botany Department, University of Queensland, John Hines Building, Brisbane, Queensland

	FEATURES	QID 4072,	Australia	Location/Qualifiers
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CDS		<1..>	1096	/EC_number="4.4.1.14" /function="conversion of ADO-MET to ACC" /note="ACC synthase"
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		/protein_id="AA04895.1"		/translation="OMGLAEINOLCFDLEDMIRKNPYASICTAEGVDEFEIYANFODY HCLPEPKAVAKFMVGRCGRVRFPDDRIATVMGGYGANEQIIIFCLADGDAFLVPSP YLPPLFDLDRGTGEIVPPCDSSSTNFOITRALPAEAREKANINIKGLITNPIS NPGLITLDRLDTLSLVSEIDEKNIHVCEBITAILFCPRKYSAVAEVYOEMDCYDL IHIVYSLSKDMGLPGFRGVIGVSYNDVAVSCIRKMSFGVLVSQTQYHLVASMLSDCEF VEFELASSKRKLARKRHIEFTKLRLEKGINCLKGNAGLFFWMDLRILLDFETVADEKKL WGTLINDVKILNSPSGSSEHCQECPMGFVCFA"
BASE COUNT		302 a	227 c	255 g 312 t
ORIGIN				
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Best Local Similarity		47.8%;	Pred. No. 1.4e+03;	
Matches	11:	Conservative	7:	Mismatches 5; Indels 0; Gaps 0;
OY	1 CANAMCKRASMNCNRSYTC 23	11 1::11::11 ::11		
Dd	1088 CAGACTCTGACCAACGAGCGTCC 1066			
RESULT 9				
AF467782/c		1097 bp	mRNA	linear PLN 18-Feb-2002
LOCUS				
DEFINITION	Prunus persica ACC synthase mRNA, partial cds.			
ACCESSION	AF467782			
VERSION	AF467782.1 GI:18699560			
KEYWORDS				
SOURCE				
ORGANISM	Prunus persica. Prunus persica Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosoid I; Rosales; Rosaceae; Amygdaloideae; Prunus. 1 (bases 1 to 1097) Yongfeng,J. and Yaozhou,Z. Cloning and expression of the peach ACC synthase gene Unpublished 2 (bases 1 to 1097)			
REFERENCE				
AUTHORS	Xiongfang,J. and yaozhou,Z.			
TITLE	Direct Submission			
JOURNAL	Submitted (15-JAN-2002) Institute of Biochemistry, Zhejiang University, Kailuan Road 268, Hangzhou, Zhejiang Province 310029, P. R. China			
REFERENCES				
LOCATION/Qualifiers				
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BASE COUNT	274	a	265	c	294	g	264	t	"MRVIVNEFLVSPGSSFRKVEPCGMFRCFA"
ORIGIN									
Query Match									66.1%: Score 15.2; DB 8; Length 1097;
Best Local Similarity									47.8%: Pred. NO. 1.4e+03;
Matches 11; Conservative									7; Mismatches 5; Indels 0; Gaps 0;
OY	1	CANANNCKRAA	MANCNRSTYC	23					
Db	1088	CATACCGCGAACCA	CCAGCGCTC	1066					
RESULT 10									
LOCUS ATU79524/c									1098 bp mRNA linear PLN 18-AUG-1998
DEFINITION Arabidopsis thaliana l-aminocyclopropane-1-carboxylate synthase									
VERSION mRNA, partial cds.									
KEYWORDS Arabidopsis thaliana.									
SOURCE Arabidopsis thaliana.									
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;									
Rosidae; eucotsids II; Brassicales; Brassicaceae; Arabidopsi									
s (bases 1 to 1098)									
Vahala,J., Schlagnhaufner,C.D. and Pell,E.J.									
Induction of an ACC synthase cDNA by ozone in light-grown									
Arabidopsis thaliana leaves									
Physiol. Plantarum 103, 45-50 (1998)									
2 (bases 1 to 1098)									
Vahala,J., Pell,E.J., Schlagnhaufner,C.D. and Arteca,R.N.									
Purification and characterization of Arabidopsis thaliana									
lipoxygenase cDNA									
Submitted 125 NOV 1996									
Diabetes 102, 109-112									
Box 28 (Viikari), Helsinki 00014, Finland									
location/Vnahlfiers									
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/codon_start=1									
/product="l-aminocyclopropane-1-carboxylate synthase"									
/protein_id="AAC32251.1"									
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/translation="OMQAEAOGLDGRKKWLKHPEASICTSEGVNOESDIATFOEDP									
H3PEPRDAVAARMEKTRNNKVRFPDPISVGATGAHEAVACIANPGKGLVPPT									
LYPPEDRLRMTRGVNLPVPCHSNGRKILVELALAEAKRSNIIPKLLTNPNT									
NPLDTTLDEKLSLVNTEIKGHILADEIYAATTFQSFIQAETIEIDECNR									
LHIVTSLSKMGHPGLRVGIVGYNDVRVOIARKMSFGVSSOTOLILAKMDSDEE									
FVDPIRESKLRIARAHELITYGDGIGLIGLKAKAGLFIMDLIRNLTKTAFDSET									
LMRTIVHQRKNVSPPGSGFHCEHGWFRCFA"									
BASE COUNT	295	a	192	c	280	g	331	t	
ORIGIN									
Query Match									66.1%: Score 15.2; DB 8; Length 1098;
Best Local Similarity									47.8%: Pred. NO. 1.4e+03;
Matches 11; Conservative									7; Mismatches 5; Indels 0; Gaps 0;
OY	1	CANANNCKRAA	MANCNRSTYC	23					
Db	1091	CATACCTGAMCAC	ARCCCGGTTC	1069					
RESULT 11									
LOCUS STU70842/c									1098 bp mRNA linear PLN 17-JAN-1998
DEFINITION Solanum tuberosum l-aminocyclopropane-1-carboxylate synthase									
(STACS5) mRNA, partial cds.									
ACCESSION U70842									
VERSION U70842.1									GI:2459544
KEYWORDS									

SOURCE Solanum tuberosum.
ORGANISM Solanum tuberosum
JOURNAL Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
REFERENCE Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
AUTHORS Asteridae; euasterids I; Solanales; Solanales; Solanales; Solanaceae; Solanum.
TITLE 1 (bases 1 to 1098)
SEQUENCE Solanum tuberosum L. leaves
SYNTHASE Sequential expression of two 1-aminocyclopropane-1-carboxylate
GENES synthase genes in response to biotic and abiotic stresses in potato
PLANT plant Mol. Biol. 35 (6), 683-688 (1997)
MEDLINE 96087996
PUBMED 9426590
2 (bases 1 to 1098)
Schlaughaufel,C.D., Arteca,R.N. and Pell,E.J.
REFERENCE Direct Submission
AUTHORS Submitted (15-SEP-1996) Horticulture, Penn State University, 103
JOURNAL Tyson Building, University Park, PA 16802, USA
TITLE Location/Qualifiers
FEATURES
SOURCE 1..1098
/organism="Solanum tuberosum"
/strain="Norland"
/db_xref="taxon:4113"
gene 1..1098
/gene="STACS5"
CDS <1..>1098
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NFUULIDKEELADLPFR INKNHILWCDLTATATAQDSFSTISVMGVCGND
LVNLSLQSDPDRDPLKGTICDQSGTITLKSNAGLFIMDLRFLENSTFNELKL
PVLEPIKSKMKCORDDPLKGTICDQSGTITLKSNAGLFIMDLRFLENSTFNELKL
LMHTINKVKLNISPGCSHFSCSPGMVRVCFPA"

BASE COUNT 362 a 169 c 226 g 341 t
ORIGIN

Query Match 66.1%; Score 15.2; DB 8; Length 1098;
Best local similarity 47.8%; Pred. No. 1.4e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Oy 1 CANANNCKRAASMANCMNRSYTC 23
||| |:::||: || |:::||
Db 1091 CATACTCTAACAACCACTGGCTC 1069

RESULT 12
AF239987/c 1100 bp mRNA linear PLN 30-MAR-2000
LOCUS
DEFINITION Prunus persica ACC synthase ACS1 mRNA, partial cds.
VERSION AF239987
KEYWORDS AF239987.1 GI:7341293
SOURCE
ORGANISM Prunus persica.
Prunus persica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
REFERENCE Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
AUTHORS Rosidae; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
TITLE 1 (bases 1 to 1100)
JOURNAL Molecular cloning and expression of peach ACC synthase gene
AUTHORS unpublished
2 (bases 1 to 1100)
Jin,Y. and Zhang,Y.
REFERENCE Direct Submission
AUTHORS Jin,Y. and Zhang,Y.
TITLE Submitted (26-FEB-2000) Institute of Biochemistry, Zhejiang
JOURNAL University, Kaiyuan Road 268, Hangzhou, Zhejiang 310029, P.R. China

	FEATURES	SOURCE
	Location/Qualifiers 1..1100 /organism="Prunus persica" /db_xref="taxon:3760"	
CDS	<1..>1100 /codon_start=1 /product="ACC synthase ACS1" /protein_id="AAf61235.1" /db_xref="GI:7341294"	
BASE COUNT	296 a 237 c 280 g 287 t	
ORIGIN		
	Query Match 66.1%; Score 15.2; DB 8; Length 1100; Best Local Similarity 47.8%; Pred. No. 1.4e+03; Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;	
OY	1 CANANNCCKRASMANCCNRSTYC 23 1::111::11::11 Db 1091 CAGACGGGAGMACCGCTGTTC 1069	
RESULT 13		
AF239989/c	AF239989 1100 bp mRNA linear PLN 30-MAR-2000	
LOCUS	Prunus persica ACC synthase ACS25 mRNA, partial cds.	
DEFINITION	AF239989	
ACCESSION	AF239989.1 GI:7341295	
VERSION		
KEYWORDS	. Prunus persica. Prunus persica. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Rosmataceae; Magnoliophyta; eudicotyledons; core eudicots; Kosidae; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus. 1 (bases 1 to 1100) Jin,Y. and Zhang,Y. Molecular cloning and expression of peach ACC synthase gene Unpublished 2 (bases 1 to 1100) Jin,Y. and Zhang,Y. Direct Submission Submitted (26-FEB-2000) Institute of Biochemistry, Zhejiang University, Kailuan Road 268, Hangzhou, Zhejiang 310029, P.R. China	
JOURNAL	Location/Qualifiers 1..1100 /organism="Prunus persica" /db_xref="taxon:3760"	
TITLE	<1..>1100 /codon_start=1 /product="ACC synthase ACS25" /protein_id="AAf61236.1" /db_xref="GI:7341296"	
AUTHORS	/translation="OMGLAENOLCPDLEIEWVLKNPEASTICVAGVNEFKDIAlFODY HGDEPERNVAANFMGKTGRNOVPFPDDRIYMSCGATGAHMTAFCLADGDALFLVPV YPFGFDLDLGMRTGVOLDIPACVSASNGEKTRALAEAKEDKNDIRKGLITMPS NLPGTVLDRETLRLSLAVFIEKKIILHLVCETIVATVESQPSIISTAIILEDIGCRN LVHVYLSLKDMGFPGFRVGIVAYSYDAVANCARKMSFELYSTOTQHLLIASLSDND EVDFEIIOSAKRLRKARMLRMTGLAQYGTSGLNGLFWMDLRQLLEKEQFEAMA LMHTIIEHWKLNVSPGSGFHPCPGEPRVCA"	
REFERENCE	LMRVIINEKLNVSPPGSFHHVEPWCVCA"	
CDS	297 a 243 c 268 g 292 t	
ORIGIN		
	Query Match 66.1%; Score 15.2; DB 8; Length 1100; Best Local Similarity 47.8%; Pred. No. 1.4e+03; Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;	
OY	1 CANANNCCKRASMANCCNRSTYC 23	

Db	1091	CACACACGACCAACCTGGCTC	1069
RESULT 14			
LOCUS	CPA012577/c	1100 bp	mrna
DEFINITION	Carica papaya mRNA for 1-aminocyclopropane-1-carboxylate synthase, partial.		linear
ACCESSION	AJ012577		PLN 07-NOV-1998
VERSION	AJ012577.1		
KEYWORDS	1-aminocyclopropane-1-carboxylate synthase; accs1 gene.		
SOURCE	Papaya.		
ORGANISM	Carica papaya		
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Caricaceae; Carica.		
AUTHORS	1 (bases 1 to 1100)		
JOURNAL	Lam, P.F.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (04-NOV-1998) Lam P.F., Biotechnology Centre, Malaysian Agricultural Research and Development Institute, GPO Box 12301, 50774 Kuala Lumpur, MALAYSIA		
TITLE	2 (bases 1 to 1100)		
JOURNAL	Lam, P.F., Tan, C.S. and Abbakar, U.K.		
REFERENCE	Nucleotide sequence of a cDNA encoding ACC synthase from ripe		
AUTHORS	Papaya fruit		
TITLE	Unpublished		
JOURNAL	Location/Qualifiers		
FEATURES	1..1100		
SOURCE	/organism="Carica papaya"		
	/cultivar="Eksotika 2"		
	/db_xref="taxon:3649"		
	/clone="pPACCS1"		
	/tissue_type="ripe fruit"		
	1..1098		
	/gene="accs1"		
	<1..>1098		
	/gene="accs1"		
	/EC_number="4.4.1.14"		
	/codon_start=1		
	/product="1-aminocyclopropane-1-carboxylate synthase"		
	/protein_id="CAI10063.1"		
	/db_xref="GI:3850657"		
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BASE COUNT	324 a	254 g	309 t
ORIGIN	213 c		
Query Match	66.1%;	Score 15.2;	DB 8;
Best Local Similarity	47.8%;	Pred. No. 1.4e+03;	
Matches 11;	Conservative	7;	Mismatches 5;
		Indels	0;
		Gaps	0;
QY	1 CANAANCKRAASMANCCNRSYTC 23		
Db	1094 CAAACACGACCAACCGAGGTTCC 1072		
RESULT 15			
LOCUS	AY120898/c	1101 bp	mrna
DEFINITION	Betula pendula 1-aminocyclopropane-1-carboxylate synthase (ACS2)		linear
ACCESSION	AY120898		
VERSION	AY120898.1		
KEYWORDS	Betula pendula.		
SOURCE	Betula pendula		
ORGANISM			

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fagales; Betulaceae; Betula.
Vahala, V., Ruonala, R., Keinänen, M., Tuominen, H. and Kangasjärvi, J.
Kinetics and signaling of ethylene, jasmonic acid and salicylic
acid modulate ozone sensitivity in birch (Betula pendula)
Unpublished
2 (bases: 1 to 1101)
Vahala, V.
Direct submission
Submitted (12-JUN-2002) Department of Biosciences, University of
Helsinki, Viikinkaari 5D FIN-00014 University of Helsinki, Finland
location/Qualifiers
1..1101
/organism="Betula pendula"
/db_xref="taxon:3505"
<1..>1101
/gene="ACS2"
/note="Bp-ACS2"
<1..>1101
/gene="ACS2"
/note="ACC synthase"
/codon_start=1
/product="1-aminocyclopropane-1-carboxylate synthase"
/protein_id="AA08089.1"
/db_xref="GI:21954116"
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NPGSTVADRELIVSVSPVNEKNHLYCDELYSATVFGSAFTSISEIIEVEYCNDD
LHIVTSLSKDMGLPGRVGLVYSNDAVYSCCKRVSSFGIVSSQTOHLASLSDDEE
FVGITLESKRLAKRKHDMFTGKERAGISCLKSNAGLFWMDLRWLEKOTFEELV
LWRVLIQVNLVSPGTFHCFHCEPGRVCFFA"

gene
CDS

BASE COUNT 281 a 230 c 289 g 301 t
ORIGIN

Query Match 66.1% Score 15.2; DB 8; Length 1101;
Best Local Similarity 47.8%; Pred. No. 1.4e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
QY 1 CANANCKRAASMANCCNRSYTC 23
||| :|||: || :|||
Db 1091 CATACGGGAGAACCAACGAGCTC 1069

Search completed: March 10, 2003, 05:57:58
Job time : 967 secs

GenCore version 5.1.4-p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 05:12:24 ; Search time 1330 Seconds
(without alignments)
280.072 Million cell updates/sec

Title: US-(9:975-842-2
Perfect score: 23
Sequence: 1 gcnyncngcngtymgtrng 23

Scoring table: IDENTITY_NUC
Gapcp:10.0 , Gapext 1.0

Searched: 16154666 segs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlmu:*
5: em_estlcv:*
6: em_estlpl:*
7: em_estlro:*
8: em_hlc:*
9: jd_estcl:*
10: qb_estcl:*
11: qb_hlc:*
12: qb_est3:*
13: qb_est4:*
14: qb_est5:*
15: en_estfun:*
16: en_estom:*
17: qd_gss:*
18: en_gss_hum:*
19: en_gss_inv:*
20: en_gss_plc:*
21: en_gss_vrt:*
22: en_gss_fun:*
23: en_gss_man:*
24: en_gss_mus:*
25: en_gss_other:*
26: en_gss_pro:*
27: en_gss_tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
C 1	15.4	67.0	103	A2309427	A2309427 1M0013K07
2	15.4	67.0	128	10	AM687380 NE009A03R
3	15.4	67.0	198	17	AL751692 Arabidops
4	15.4	67.0	332	14	Z33841 ATTS2940 St
5	15.4	67.0	351	9	AU092777
6	15.4	67.0	428	10	AV410488 AV410488

7	15.4	67.0	421	12	BP112525	BP112525 EST440115
8	15.4	67.0	430	9	AI898708	AI898708 EST268151
9	15.4	67.0	438	10	BE458995	BE458995 EST414287
10	15.4	67.0	479	14	N65643	N65643 20683 Lambd
11	15.4	67.0	487	17	BH803717	BH803717 100810380
12	15.4	67.0	496	9	AI193687	AI193687 701497137
13	15.4	67.0	505	9	AA650853	AA650853 30967 Lam
14	15.4	67.0	519	12	BF276958	BF276958 GA_Eb002
15	15.4	67.0	521	9	AI189837	AI189837 EST268280
16	15.4	67.0	522	13	BI135805	BI135805 sa63e08.
17	15.4	67.0	537	9	AI1894662	AI1894662 EST264105
18	15.4	67.0	552	14	BO696008	BO696008 NXPV_035
19	15.4	67.0	595	9	AI897818	AI897818 EST267261
20	15.4	67.0	607	17	B61942	B61942 T19L13FR TA
C 21	15.4	67.0	610	17	AZ304558	AZ304558 1M0004108
22	15.4	67.0	632	9	AI485339	AI485339 EST243720
23	15.4	67.0	636	9	AI485332	AI485332 EST243653
24	15.4	67.0	637	10	AW441375	AW441375 EST310771
25	15.4	67.0	651	12	BF649567	BF649567 NE079G12E
26	15.4	67.0	656	9	AL505273	AL505273 AL505273
27	15.4	67.0	658	9	AI487009	AI487009 EST245331
28	15.4	67.0	672	9	AI898099	AI898099 EST267542
29	15.4	67.0	675	10	BB624474	BB624474 BB624474
30	15.4	67.0	676	9	AU175348	AU175348 AU175348
31	15.4	67.0	704	13	BI921893	BI921893 EST41726
32	15.4	67.0	705	13	BM412805	BM412805 EST567132
C 33	15.4	67.0	803	17	BH708432	BH708432 B0HTU20TF
34	15.4	67.0	804	17	BH653915	BH653915 B0MT146TF
35	15.4	67.0	819	13	BI421967	BI421967 EST352653
36	15.4	67.0	839	14	BM779146	BM779146 EST389721
37	15.4	67.0	851	17	BH517344	BH517344 B0GRK16TF
C 38	15.4	67.0	936	13	BM451926	BM451926 AGENCOURT
39	15.4	67.0	952	17	AZ209422	AZ209422 SP_0106_A
40	15.4	67.0	1101	17	AL050471	AL050471 Drosophill
41	15.4	67.0	1101	17	CNS00202	AL063501 Drosophill
42	15.4	67.0	1588	11	AY104732	AY104732 zea mays
43	14.4	62.6	161	13	BM498038	BM498038 952021C08
44	14.4	62.6	235	10	AV379564	AV379564 AV379564
C 45	14.4	62.6	241	10	AV321580	AV321580 AV321580

ALIGNMENTS

RESULT 1
A2309427/ C 103 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0013K07R Mouse 10kb Plasmid UNGC1M library Mus musculus genomic
clone UNGC1M0013K07 R, DNA sequence.

ACCESSION A2309427.1 GI:10350398
VERSION
KEYWORDS
SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0013 row: K column: 07
 Seq primer: CACACGGAACAGCATGACC
 Class: Plasmid ends
 High quality sequence stop: 103.

FEATURES

source

1. 103
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCGM013K07"
 /clone_1lb="Mouse 10Kb plasmid UUCGM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 16 a 41 c 21 g 25 t
 ORIGIN

Query Match 67.0%; Score 15.4; DB 17; Length 103;
 Best Local Similarity 56.5%; Pred. No. 1.4e+03;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 Oy 1 GGNATCCGCGTTCAGCATGG 23
 ||:|||||:|:|:|:|:|:|
 Db 83 GGACGCTCGGTTCAGCATGG 61

RESULT 2 128 bp mRNA linear EST 20-DEC-2000
 AM687380
 LOCUS NF009A03RT1F1019 Developing root Medicago truncatula cDNA clone
 DEFINITION NF009A03RT 5', mRNA sequence.
 ACCESSION AM687380
 VERSION AM687380.2 GI:11928221
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
 1 (bases 1 to 128)
 Watson,B.S., Shin,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R.,
 Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May
 G.D. and Paiva,N.L.
 'Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 Medicago truncatula root library
 Unpublished (2000)
 On Apr 14, 2000 this sequence version replaced g1:7562116.
 CONTACT: Paiva NL
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7317
 Fax: 580 221 7380
 Email: n.paiva@noble.org

Insert Length: 768 Std Error: 0.00
 Plate: 009 row: A column: 03
 Seq primer: TCACACGGAACAGCATGAC.
 Location/Qualifiers

FEATURES

source

1. 128
 Location/Qualifiers
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="NF009A03RT"
 /clone_1lb="Developing root"
 /issue_type="root"
 /dev_stage="Pooled developmental"
 /note="Vector: Lambda Zap; Total RNA was extracted from non-modulated roots of plants grown in 1 mM nitrate medium. Samples were taken at four time points (approximately two days, one, two and six weeks post germination) representing early seedling growth to nitrogen limitation."

BASE COUNT 43 a 22 c 20 g 43 t
 ORIGIN

Query Match 67.0%; Score 15.4; DB 10; Length 128;
 Best Local Similarity 56.5%; Pred. No. 1.5e+03;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 Oy 1 GGNATCCGCGTTCAGCATGG 23
 ||:|||||:|:|:|:|:|:|
 Db 82 GGATTCCTCGTTTACGATTGG 104

RESULT 3 198 bp DNA linear GSS 17-JUN-2002
 AL751692
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-006E12-014808,
 DEFINITION genomic survey sequence.
 ACCESSION AL751692
 VERSION AL751692.1 GI:21484190
 KEYWORDS GSS.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
 and Weissshaar,B.
 A pipeline for automated high-throughput generation of ESTs
 (flanking sequence tags) from Arabidopsis thaliana T-DNA
 transformed lines
 Unpublished
 2 Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weissshaar,B.
 A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
 for flanking sequence tag based reverse genetics
 Unpublished
 3 (bases 1 to 198)
 Strizhov,N., Li,Y., Rosso,M. and Weissshaar,B.
 Direct Submission
 Submitted (17-JUN-2002) Weissshaar B., Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence is recovered from the left border of the T-DNA. It
 indicates an insertion close to or within gene At3g61510. The
 sequences are generated at the MPI for Plant Breeding Research in
 the context of the GABI-Kat project. GABI-Kat is part of the German
 Plant Genomics program designated 'GABI'. Information on line
 availability can be found at:
 http://www.mpi-zkoeln.mpg.de/GABI-Kat/.

FEATURES

source

1. 198
 Location/Qualifiers
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-006E12-014808"
 /clone_1lb="Arabidopsis thaliana T-DNA insertion lines"

BASE COUNT	44 a	38 c	48 g	68 t	
ORIGIN	removed"				
Query Match	57.0%;	Score 15.4;	DB 17;	Length 198;	
Best Local Similarity	56.5%;	Pred. No. 1.6e+03;			
Matches 13;	Conservative 4;	Mismatches 6;	Indels 0;	Gaps 0;	
OY	1 GGNATNCNGGNTTYMGNRING 23				
Db	77 GGTCTCCCGCTTCGCGGTGG 99				
RESULT 4					
LOCUS	233841	332 bp	mrna	linear	EST 25-MAY-1994
DEFINITION	ATRS2940 Strasbourg-A Arabidopsis thaliana clone FAI88 5',				
ACCESSION	233841				
VERSION	233841.1				
KEYWORDS	EST.				
SOURCE	thale cress.				
ORGANISM	Arabidopsis thaliana				
REFERENCE	Eukaryot; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Brassicales; Brassicaceae; Arabidopsis.				
AUTHORS	1 (bases 1 to 332)				
JOURNAL	CNRS				
COMMENT	The Arabidopsis thaliana transcribed genome: the GDR cDNA program				
LOCUS	unpublished (1996)				
CONTACT	Gigot Claude / L512 C.				
LABORATORY	Laboratoire de Biologie Molculaire des Plantes - CNRS				
EMAIL	12 Rue du General Zimmer, 67084 Strasbourg Cedex, France				
LOCATION/Qualifiers	Email: ALABANK@EDC.U-STRASBG.FR.				
FEATURES	Source				
LOCUS	1. 332				
DEFINITION	/organism="Arabidopsis thaliana"				
ACCESSION	/db_xref="ecolype:Columbia"				
VERSION	/db_xref="taxon:3702"				
KEYWORDS	/clone="FAI88"				
SOURCE	/clone_lib="Strasbourg-A"				
ORGANISM	/note="Vector: Lambda ZAPII; tissue=sliced leaves of A. thaliana ecotype Columbia; clone_library=Strasbourg-A; Cloning vector: Lambda ZAPII; Physiological condition: Leaves strips incubated 2/3/4 days in liquid culture medium."				
BASE COUNT	86 a	84 c	82 g	78 t	2 others
ORIGIN					
Query Match	67.0%;	Score 15.4;	DB 14;	Length 332;	
Best Local Similarity	56.5%;	Pred. No. 1.8e+03;			
Matches 13;	Conservative 4;	Mismatches 6;	Indels 0;	Gaps 0;	
OY	1 GGNATNCNGGNTTYMGNRING 23				
Db	281 GGTCTCTCGTTCGCGGTGG 303				
RESULT 5					
LOCUS	AN092777	351 bp	mrna	linear	EST 03-APR-2002
DEFINITION	AN092777 rice callus Oryza sativa (japonica cultivar-group) cDNA				
ACCESSION	clone C5337, mrna sequence.				
ORIGIN					
Query Match	67.0%;	Score 15.4;	DB 14;	Length 332;	
Best Local Similarity	56.5%;	Pred. No. 1.8e+03;			
Matches 13;	Conservative 4;	Mismatches 6;	Indels 0;	Gaps 0;	
OY	1 GGNATNCNGGNTTYMGNRING 23				
Db	281 GGTCTCTCGTTCGCGGTGG 303				
RESULT 6					
LOCUS	AV410488	428 bp	mrna	linear	EST 23-MAY-2000
DEFINITION	AV410488 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MW1073e12_r 5', mrna sequence.				
ACCESSION	AV410488				
VERSION	AV410488.1				
KEYWORDS	GI:7723342				
SOURCE	EST.				
ORGANISM	Lotus japonicus.				
REFERENCE	Lotus japonicus.				
AUTHORS	1 (bases 1 to 428)				
TITLE	Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.				
JOURNAL	Generation of 7137 non-redundant expressed sequence tags from a				
MEDLINE	legume, Lotus japonicus				
COMMENT	DNA Res. 7 (2), 127-130 (2000)				
CONTACT	20277479				
LABORATORY	Contact: Yasukazu Nakamura				
EMAIL	The First Laboratory for Plant Gene Research				
LOCATION/Qualifiers	kazusa DNA Research Institute				
LOCATION/Qualifiers	Yana 1532-3, Kisarazu, Chiba 292-0812, Japan				
LOCATION/Qualifiers	Email: ynakamukazusa.or.jp, URL: http://www.kazusa.or.jp/en/plan/.				
LOCUS	1. 428				
DEFINITION	/organism="Lotus japonicus"				
ACCESSION	/db_xref="taxon:34305"				
VERSION	/clone="MW1073e12_r"				
KEYWORDS	/clone_lib="Lotus japonicus young plants (two-week old)"				
SOURCE					
Query Match	67.0%;	Score 15.4;	DB 9;	Length 351;	
Best Local Similarity	56.5%;	Pred. No. 1.9e+03;			
Matches 13;	Conservative 4;	Mismatches 6;	Indels 0;	Gaps 0;	
OY	1 GGNATNCNGGNTTYMGNRING 23				
Db	298 GGTCTCCCGCTTCGCGGTGG 320				
RESULT 7					
LOCUS	AV410488	428 bp	mrna	linear	EST 23-MAY-2000
DEFINITION	AV410488 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MW1073e12_r 5', mrna sequence.				
ACCESSION	AV410488				
VERSION	AV410488.1				
KEYWORDS	GI:7723342				
SOURCE	EST.				
ORGANISM	Lotus japonicus.				
REFERENCE	Lotus japonicus.				
AUTHORS	1 (bases 1 to 428)				
TITLE	Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.				
JOURNAL	Generation of 7137 non-redundant expressed sequence tags from a				
MEDLINE	legume, Lotus japonicus				
COMMENT	DNA Res. 7 (2), 127-130 (2000)				
CONTACT	20277479				
LABORATORY	Contact: Yasukazu Nakamura				
EMAIL	The First Laboratory for Plant Gene Research				
LOCATION/Qualifiers	kazusa DNA Research Institute				
LOCATION/Qualifiers	Yana 1532-3, Kisarazu, Chiba 292-0812, Japan				
LOCATION/Qualifiers	Email: ynakamukazusa.or.jp, URL: http://www.kazusa.or.jp/en/plan/.				
LOCUS	1. 428				
DEFINITION	/organism="Lotus japonicus"				
ACCESSION	/db_xref="taxon:34305"				
VERSION	/clone="MW1073e12_r"				
KEYWORDS	/clone_lib="Lotus japonicus young plants (two-week old)"				
SOURCE					
Query Match	67.0%;	Score 15.4;	DB 9;	Length 351;	
Best Local Similarity	56.5%;	Pred. No. 1.9e+03;			
Matches 13;	Conservative 4;	Mismatches 6;	Indels 0;	Gaps 0;	
OY	1 GGNATNCNGGNTTYMGNRING 23				
Db	298 GGTCTCCCGCTTCGCGGTGG 320				
RESULT 8					
LOCUS	AV410488	428 bp	mrna	linear	EST 23-MAY-2000
DEFINITION	AV410488 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MW1073e12_r 5', mrna sequence.				
ACCESSION	AV410488				
VERSION	AV4104				

/dev-stage="young plants (two-week old)"
 /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
 XhoI; Isolate=MIYAKOJima MG-20"

BASE COUNT 133 a 116 c 80 g 99 t

ORIGIN

Query Match 67.0%; Score 15.4; DB 10; Length 428;
 Best Local Similarity 56.5%; Pred. No. 1.9e+03;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNATNCNGNGNTYMGNTNGG 23

DB 374 GGGTTCCTCGATTTCAGACTGG 396

RESULT 7
 BFL12525 431 bp mRNA linear EST 18-MAY-2001

LOCUS BFL12525 tomato breaker fruit Lycopersicon esculentum cDNA clone
 DEFINITION EST140115 5' sequence, mRNA sequence.

ACCESSION BFL12525
 VERSION BFL12525.1 GI:10942215

KEYWORDS EST

SOURCE tomato.
 ORGANISM Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

Lycopersicon.
 1 (bases 1 to 431)

Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
 Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Rønning,C.M.,
 Niernan,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,
 S.D.
 Generation of ESTs from tomato fruit tissue, breaker stage

Unpublished (2000)

CONTACT: CUGI
 Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>.

Location/Qualifiers

1..431
 /organism="Lycopersicon esculentum"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="CLEG41J5"
 /clone_lib="tomato breaker fruit"
 /tissue_type="pericarp"
 /dev_stage="breaker"
 /lab_host="SOLR"

/note="Vector: pBluescriptSKmCunadap; Site_1: EcoRI;
 Site_2: XhoI; supplier: Boyce Thompson Institute;
 sequencing: The Institute for Genomic Research. Fruit
 were harvested at the breaker stage (first sign of
 lycopen accumulation on the blossom end of fruit). Fruit
 were cut in half and the seeds and locules were discarded
 prior to freezing the pericarp."

BASE COUNT 132 a 76 c 82 g 141 t

ORIGIN

Query Match 67.0%; Score 15.4; DB 12; Length 431;
 Best Local Similarity 56.5%; Pred. No. 1.9e+03;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNATNCNGNGNTYMGNTNGG 23

DB 232 GGGTTCCTCGATTTCAGACTGG 254

RESULT 8
 A1898708 450 bp mRNA linear EST 18-MAY-2001

LOCUS A1898708

DEFINITION EST268151 tomato ovary, TAMU Lycopersicon esculentum cDNA clone
 CLEP35K4, mRNA sequence.

ACCESSION A1898708
 VERSION A1898708.1 GI:5604610

KEYWORDS EST

SOURCE

tomato.
 Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

Lycopersicon.
 1 (bases 1 to 450)

Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E.,
 Liang,F., Upton,J., Rønning,C.M., Craven,M.B., Fujii,C.Y., Bowman,
 C.L., Niernan,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,
 S.D. and Giovannoni,J.
 Generation of ESTs from tomato carpel tissue

Unpublished (1999)

CONTACT: CUGI
 Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 5 prime sequence.

Location/Qualifiers

1..450
 /organism="Lycopersicon esculentum"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="CLEP35K4"
 /clone_lib="tomato ovary, TAMU"
 /tissue_type="carpel"
 /dev_stage="5 days pre-anthesis to 5 days post-anthesis"
 /lab_host="XLI-Blue Wfr"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI; cled - Tomato Carpel EST library. OligoT-primed and
 directionally cloned cDNA in vector Lambda Zap II with 5'
 and 3' ends located at the EcoRI and XhoI sites,
 respectively."

BASE COUNT 146 a 81 c 84 g 139 t

ORIGIN

Query Match 67.0%; Score 15.4; DB 9; Length 450;
 Best Local Similarity 56.5%; Pred. No. 2e+03;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNATNCNGNGNTYMGNTNGG 23

DB 421 GGAATTCAGACTTCAGACTTCG 443

RESULT 9
 BE458995 459 bp mRNA linear EST 18-MAY-2001

LOCUS BE458995
 DEFINITION EST414287 tomato developing/immature green fruit Lycopersicon
 esculentum cDNA clone CLEM5013, mRNA sequence.

ACCESSION BE458995
 VERSION BE458995.1 GI:9503297

KEYWORDS EST

SOURCE

tomato.
 Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

Lycopersicon.
 1 (bases 1 to 459)

Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
 Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Rønning,C.M.,
 Niernan,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,
 S.D.
 Generation of ESTs from tomato fruit tissue, immature green

Unpublished (2000)
 CONTACT: CUGI

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES

Location/Qualifiers
1..459

BASE COUNT 165 a 80 c 135 t
ORIGIN
Query Match 67.0%; Score 15.4; DB 10; Length 459;
Best Local Similarity 56.5%; Pred. No. 2e+03;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGNATCCGCGTTCGTTAGGTTGG 23
Db 320 GGGTTCTCTGATTTAGGTTGG 342

RESULT 10
LOCUS N65643 479 bp mRNA linear EST 05-JAN-1998
DEFINITION 20683 Lambda-PRL2 Arabidopsis thaliana cDNA clone 2401277, mRNA
ACCESSION N65643
VERSION N65643.1 GI:1217269
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 479)
Neman, T., deBull, F. J., Green, P., Keegstra, K., Kende, H., McIntosh,
L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Reisel,
E., and Somerville, C.
Gene source: a summary of methods for accessing results from
large scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
COMMENT
CONTACT: Thomas Newman
MSU/DOE Plant Research Laboratory
Michigan State University
MSU/DOE Plant Research Laboratory, Plant Biology Bldg. E.
East Lansing, Michigan 48824
Tel: 517-383-0854
Fax: 517-383-9168
Email: neuman@plant.msu.edu
Seq primer 47 dyp primer
Location/Qualifiers
1..479

FEATURES

Source
/organism="Arabidopsis thaliana"
/strain="var. columbia"
/db_xref="taxon:3702"
/clone_lib="lambda-prl2"
/note="Vector: lambda Zip-lox; Site 1: Sal; Site 2: Not;
Lambda prl2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture

grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark-rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques). The vector is BRL's lambda Zip-lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
0.190 dt primed cDNA.
BASE COUNT 106 a 97 c 121 g 136 t 19 others
ORIGIN

Query Match 67.0%; Score 15.4; DB 14; Length 479;
Best Local Similarity 56.5%; Pred. No. 2e+03;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGNATCCGCGTTCGTTAGGTTGG 23
Db 180 GGTCTCTCTGATTTAGGTTGG 202

RESULT 11
LOCUS BH803717 487 bp DNA linear GSS 25-APR-2002
DEFINITION 1008103H01.x1 1008 - Rescuedu Grid I Zea mays genomic, DNA
sequence.
ACCESSION BH803717
VERSION BH803717.1 GI:20319176
KEYWORDS GSS.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 487)
Walbot, V.
Maize genomic sequences found using engineered Rescuedu transposon
unpublished (2001)
CONTACT: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008103 row: 5
Class: transposon-tagged.
Location/Qualifiers
1..487

FEATURES
Source
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1008 - Rescuedu Grid I"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: leaf; Vector: Rescuedu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
Rescuedu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on Rescuedu, go to the web
site www.zmdb.lasalle.edu and follow the links for
Rescuedu. Grid I was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin.

BASE COUNT 69 a 165 c 172 g 81 t
ORIGIN

Query Match 67.0%; Score 15.4; DB 17; Length 487;
Best Local Similarity 56.5%; Pred. No. 2e+03;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Search completed: March 10, 2003, 06:42:37
 Job time : 1343 secs

```

/cultivar="8400"
/db_xref="taxon:29729"
/clone_1ib="E80026C04f"
/clone_1ib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa host="E. coli"
/notes="vector: pBR-CMV; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT      154 a      83 c      113 g      169 t
ORIGIN

Query Match
Best Local Similarity 56.5%; Score 15.4; DB 9; Length 519;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

1 GGNATCGCGGNTVMGNRTNG 23
||:|||||:|||||:|||||
Db 133 GGGTCCCTCGGTTTAGAGTTGG 155

RESULT 15
A1898837 521 bp mRNA linear EST 18-MAY-2001
LOCUS EST268280 tomato ovary, TAMU Lycopersicon esculentum cDNA clone
DEFINITION CLE035F22 mRNA sequence.
ACCESSION A1898837
VERSION A1898837.1 GI:5604739
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 521)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Romning,C.M., Craven,M.B., Fujii,C.Y., Bowman,
C.D., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley
S.D. and Giovannoni,J.
Generation of ESTs from tomato carpel tissue
Unpublished (1999)
Contact: CBGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.

FEATURES
source
Location/Qualifiers
1..521
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CLE035F22"
/clone_1ib="tomato ovary, TAMU"
/tissue_type="carpel"
/dev_stage="5 days pre-anthesis to 5 days post-anthesis"
/lab_host="XLI-Blue MRF"
/notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; CLE03 - tomato Carpel EST Library. OligodT-primed and
directionally cloned cDNA in vector Lambda ZAP II with 5'
and 3' ends located at the EcoRI and XhoI sites,
respectively. 98 g 155 t

BASE COUNT      175 a      93 c      98 g      155 t
ORIGIN

Query Match
Best Local Similarity 56.5%; Score 15.4; DB 9; Length 521;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

1 GGNATCGCGGNTVMGNRTNG 23
||:|||||:|||||:|||||
Db 399 GGATTCAGATTCAGATTGG 421

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```

/clone_lib="TREC CNW Wheat Powderly Mildew Resistant
Library"
/tissue_type="leaf"
/dev_stage="seedling, challenged with powdery mildew
strain"
/note="Vector: Lambda Triplex Site_1: Still Primer used:
5'-TCGAGACTGCGAGCAGC-3' 500 bp average Insert size."
BASE COUNT      53 a      99 c      101 g      44 t      3 others
ORIGIN

Query Match      66.1%; Score 15.2; DB 10; Length 300;
Best Local Similarity 52.2%; Pred. No. 1.9e+03;
Matches 12; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

OY      1 CANANCKRRAASMANCNRSTYC 23
Db      125 CAGAGCGGAGACACACGCGGCTC 103

RESULT 4
LOCUS      BM149376/c      342 bp      mRNA      linear      EST 30-NOV-2001
DEFINITION      TCAP2011991 Pediatric acute myelogenous leukemia cell (FAB M1)
Baylor-H3SC Project-TCOA Homo sapiens cDNA clone TCAP1199, mRNA
sequence.
ACCESSION      BM149376
VERSION      BM149376.1 GI:17170934
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 342)
AUTHORS      Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman,F.R. Jr.,
Gunnarsson,P.H., Murthy,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.
Pediatric acute leukemia cDNA Sequencing Project (2001)
JOURNAL      Unpublished (2001)
COMMENT      Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
1102 Barnes, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: c.gibbs@tccc.org
Seq primer: M13 primer.
FEATURES
Source
Location/Qualifiers
1..342
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="TCAP1199"
/clone_lib="Pediatric acute myelogenous leukemia cell (FAB
M1) Baylor-H3SC Project-TCOA"
/sex="male"
/tissue_type="leukophoresis"
/cell_type="myeloid cell"
/dev_stage="pediatric 6 years"
/lab_host="DH10B"
/note="Vector: lambda PSB, Site_1: BamHI; Site_2: EcoRI;
First strand cDNA was primed with an anchored
XhoI-oligo(dT) primer [5'GGAGACTGCGAGCGCGAGAG(1)VN
3', V-A,C,G; N-A,C,G,T] and then dg tailed. Second strand
was primed with a BamHI-dc primer
[5'AGAGACTGCGATCGCGCGCAATAAATAAAT(C) 3'1.
Double-stranded cDNA was then digested with BamHI and XhoI
and directionally cloned into the BamHI and SalI sites of
lambda PSB vector. Library went through one round of
normalization. Library was constructed by Wei Yu at RIKEN
of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,
Itoh M, Nagaoka S, Sasaki N, Okazaki Y, Muramatsu M,
Schneider C, Hayashizaki Y, High efficiency selection of
full-length cDNA by improved biotinylated cap trapper.,
DNA Res 4: 1, 61-6, Feb 28, 1997)"
BASE COUNT      51 a      100 c      94 g      97 t

```

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ORIGIN

Query Match      66.1%; Score 15.2; DB 13; Length 342;
Best Local Similarity 47.8%; Pred. No. 2e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY      1 CANANCKRRAASMANCNRSTYC 23
Db      275 CAGAGCGGAGACACACGCGGCTC 253

RESULT 5
LOCUS      Z34718      351 bp      mRNA      linear      EST 11-JUL-1994
DEFINITION      ATTS3478 Strasbourg-A Arabidopsis thaliana cDNA clone FA188 3',
mRNA sequence.
ACCESSION      Z34718
VERSION      Z34718.1 GI:507023
KEYWORDS      EST.
SOURCE      The Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 351)
CNRS.
The Arabidopsis thaliana transcribed genome: the GDR cDNA program
Unpublished (1996)
Contact: Philippe G., Gigot C.
Gigot Claude / L512
Laboratoire de Biologie Molculaire des Plantes - CNRS
12 Rue du General Zimmer, 67084 Strasbourg Cedex, France
Email: ARABANK@MEDOC.U-STRASBG.FR.
FEATURES
Source
Location/Qualifiers
1..351
/organism="Arabidopsis thaliana"
/strain="ecotype Columbia"
/db_xref="taxon:3702"
/clone="FA188"
/clone_lib="Strasbourg-A"
/note="Vector: Lambda ZAP11; tissue-sliced leaves of
A. thaliana ecotype columbia; clone library-Strasbourg-A;
Cloning vector: lambda ZAP11; physiological condition:
leaves strips incubated 2/3/4 days in liquid culture
medium."
BASE COUNT      131 a      79 c      30 g      110 t      1 others
ORIGIN

Query Match      66.1%; Score 15.2; DB 14; Length 351;
Best Local Similarity 47.8%; Pred. No. 2e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY      1 CANANCKRRAASMANCNRSTYC 23
Db      327 CAAACCTTAACATCGACCTC 349

RESULT 6
LOCUS      AQ207050      360 bp      DNA      linear      GSS 17-SEP-1998
DEFINITION      HS_3242_A2.G04_MR_CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate-3242 Col-8 Row-M, DNA sequence.
ACCESSION      AQ207050
VERSION      AQ207050.1 GI:3617620
KEYWORDS      GSS.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 360)
AUTHORS      Mahliras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,D., Young,D., Zhao,S., Adams,M.D. and
Hood,L.

```

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3242 row: M column: 8
Class: BAC ends
High quality sequence stop: 360.

FEATURES
Source location/Qualifiers
1..360
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="plate:3242 Col=8 Row=M"
/note="Organ: C1T Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 69 a 132 c 45 g 112 t 2 others

ORIGIN
Query Match 66.1%; Score 15.2; DB 17; Length 360;
Best Local Similarity 47.8%; Pred. No. 2e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CANANCKRAASMANCCNRSTYC 23
||| 1:||||:111:||||
Db 302 CATAGTCGACACATCCTACCTC 324

RESULT 7
A1608175/c 361 bp mRNA linear EST 21-APR-1999
LOCUS A1608175
DEFINITION v683h10.y1 Ko mouse embryo 11 5dpc Mus musculus cDNA clone
IMAGE:789667 5' similar to TR:063418 Q63418 PROTOCADHERIN 3. ;
mRNA sequence.
A1608175
A1608175.1 GI:4617342
EST.
house mouse.
house musculus
ORGANISM Mus musculus
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 361)
Matta,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Waller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
The Washu-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/Washu-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:474075
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the correct orientation)
Possible reversed clone; similarity on wrong strand
Seq primer: Primer name ambiguous
High quality sequence stop: 161.
location/Qualifiers

FEATURES
Source location/Qualifiers

source 1..361
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_id="IMAGE:789667"
/clone_lib="Ko mouse embryo 11 5dpc"
/sex="pooled"
/tissue_type="embryo"
/dev_stage="11.5dpc"
/lab_host="DH10B"
/note="Organ: embryo; Vector: pSPORT1; Site 1: SalI; Site 2: NotI; Total RNAs were extracted from 11.5 dpc embryos (excluding placenta and yolk sac). The double-stranded cDNA was synthesized with an oligo (dT)-1 primer GAGAGGACTAGTTCAGATCGGACGGCGCTTTT TTTT TTTT 3'. The cDNAs were ligated to LL-Sal3A: 5' GCTATGACCTCGACATATC 3' and LL-Sal3B: 5' GATAGTCGACGTCAT 3'. The cDNAs were size-selected and amplified by long-range PCR using Ex Taq polymerase for 18 cycles. The PCR-amplifiable cDNA mixture went through one round of equalization and was digested with SalI/NotI and cloned into the SalI/NotI sites of the pSPORT1 plasmid vector (Life Technologies). The library was constructed by Dr. Minoru S. H. Ko and Dr. Xiaohong Wang."

BASE COUNT 69 a 107 c 105 g 78 t 2 others

ORIGIN
Query Match 66.1%; Score 15.2; DB 9; Length 361;
Best Local Similarity 47.8%; Pred. No. 2e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CANANCKRAASMANCCNRSTYC 23
||| 1:||||:111:||||
Db 168 CACACCTGAACACCCGCGCTC 146

RESULT 8
BE353050/c 406 bp mRNA linear EST 19-JUL-2000
LOCUS BE353050
DEFINITION DG1_3_F05.g1_A002 Dark Grown 1 (DG1) Sorghum bicolor cDNA, mRNA
sequence.
BE353050
ACCESSION BE353050.1 GI:9281026
VERSION BE353050.1
KEYWORDS EST.
Sorghum.
ORGANISM Sorghum bicolor
SOURCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 406)
Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt,L.H.
An EST database from Sorghum: dark-grown seedlings
Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.
Seq primer: 77
High quality sequence start: 36
High quality sequence stop: 406
POLYA=Yes.
location/Qualifiers
1..406
/organism="Sorghum bicolor"
/db_xref="taxon:4558"

FEATURES
Source location/Qualifiers

```

/clone.lib="Dark Grown 1 (DGI)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
lambda zap; Site-1: XhoI; Site-2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
BASE COUNT      105 a      88 c      117 g      96 t
ORIGIN
Query Match      66.1%; Score 15.2; DB 10; Length 406;
Best Local Similarity 47.8%; Pred. No. 2.2e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY      1 CANANCKR2ASMANCNRSTC 23
Db      135 CACACCGCTGACCGCGGCTC 113

RESULT 9
BE209956/c      410 bp      mRNA      linear      EST 04-DEC-2001
LOCUS      so37b07.y1 Gm-cl039 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
DEFINITION      Gm-cl035-110 5' similar to FR:Q43201 Q43201
1-AMINOXYLOPROPANE-1-CARBOXYLATE SYNTHASE ; mRNA sequence.
ACCESSION      BE209956
VERSION      BE209956.1 GI:8825235
KEYWORDS      EST
SOURCE      soybean
ORGANISM      Glycine max
REFERENCE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 410)
Shoemaker,R., Keum,P., Vodkin,L., Expelling,J., Coryell,V., Khanna
,A., Bolla,B., Marita,M., Hillier,L., Kucaba,T., Martin,D., Beck,C.,
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Persop,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Rilter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Watkinson,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: curesgen.com
Insert Length: 1204 Std Error: 0.00
High quality sequence stop: 409.
Location/Qualifiers
1. 410
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl039-110"
/clone.lib="Gm-cl039"
/tissue.type="whole seedling without cotyledons"
/lab.host="DH10B"
/note="vector: pBluescriptII SK+; Site-1: EcoRI; Site-2:
XhoI; This cDNA library was constructed from mRNA isolated
from 2 week old seedlings with the cotyledons removed at
the time of harvest. The seedlings for the cultivar Ogden
were grown in a growth chamber using germination paper.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with a XhoI restriction
site. EcoRI adapters were ligated to the blunt-ended cDNA
fragments followed by XhoI digestion. The cDNA fragments
were directionally cloned into the EcoRI-XhoI restriction
site of the pBluescript vector. The ligated cDNA fragments
were transformed into DH10B host cells (Gibco BRL). This

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library was constructed by Dr. Randy Shoemaker."
BASE COUNT      97 a      72 c      110 g      130 t
ORIGIN
Query Match      66.1%; Score 15.2; DB 10; Length 410;
Best Local Similarity 47.8%; Pred. No. 2.2e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY      1 CANANCKR2ASMANCNRSTC 23
Db      323 CAAACAGCAACATCCGCGCTC 301

RESULT 10
AL502553
LOCUS      AL502553      413 bp      mRNA      linear      EST 04-JAN-2001
DEFINITION      AL502553 Hordeum vulgare Barke roots Hordeum vulgare cDNA clone
HM07P07u 3', mRNA sequence.
ACCESSION      AL502553
VERSION      AL502553
KEYWORDS      EST
SOURCE      Hordeum vulgare.
ORGANISM      Hordeum vulgare.
REFERENCE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
TITLE      ; Tricase; Hordeum.
1 (bases 1 to 413)
Michael,W., Meschke,W., Pleissner,K.-P. and Graner,A.
EST sequencing and analysis in barley
Unpublished (2000)
Contact: Michael W
Institute for Plant Genetics and Crop Plant Research
Corrensstr.3, D-06466 Gatersleben, Germany
Email: michael@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: M13mt primer for 3' end.
Location/Qualifiers
1. 413
/organism="Hordeum vulgare"
/cultivar="Barke"
/db_xref="taxon:4513"
/clone="HM07P07u"
/clone.lib="Hordeum vulgare Barke roots"
/tissue.type="roots"
/lab.host="XL01R"
/note="vector: Plasmid pRK-CMV; Site-1: EcoRI; Site-2:
XhoI; mRNA was made from roots of spring barley variety
'Barke', a high quality malting variety. Roots were grown
for two days on filter paper at room temperature. Cloning
sites: EcoRI (3'-end of cDNA) and XhoI (3'-end of cDNA).
NOTE: Due to a cloning artefact caused by the K1L in most
cases the EcoRI site is NOT present, as well as the EcoRI
adapter. Average insert size is 1 kb. Sequence trimming:
Vector sequences and sequence ends were trimmed from the
5'- and 3'-end until a 50 bp window contains less than two
ambiguities. The maximum length was set to 700 bp."
BASE COUNT      84 a      116 c      92 g      121 t
ORIGIN
Query Match      66.1%; Score 15.2; DB 9; Length 413;
Best Local Similarity 47.8%; Pred. No. 2.2e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY      1 CANANCKR2ASMANCNRSTC 23
Db      256 CACACCGCTGACCGCGCTC 278

RESULT 11
AV820681
LOCUS      AV820681      420 bp      mRNA      linear      EST 01-APR-2002
DEFINITION      AV820681 RAPFL1 Arabidopsis thaliana cDNA clone RAPFL1-1-L09 3',
mRNA sequence.
ACCESSION      AV820681

```

VERSION AV820681.1 GI:19862660
 KEYWORDS EST.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 420)
 REFERENCE Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
 Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
 Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.,
 and Shinozaki, K.
 Large scale analysis of Arabidopsis full-length cDNA (2002b)
 JOURNAL Unpublished (2002)
 COMMENT Contact: Motoaki Seki
 Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060
 Email: mseki@rc.riken.go.jp
 An Arabidopsis full-length cDNA library was constructed essentially
 as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
 and XhoI was ligated to modified lambda phage-1 vector (Carninci et
 al., submitted for publication) digested with BamHI and SalI. This
 clone is in a modified phagescript vector. Please visit our web
 site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
 details.

FEATURES
 source Location/Qualifiers
 1..420
 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"
 /clone="RAFL11-11-L09"
 /clone_1lb="RAFL11"
 /dev_stage="plants at various developmental stages from
 germination to mature seeds"
 /lab_host="DH10B"
 /note="Site_1: BamHI; Site_2: SalI; subjected to various
 treatments (dehydration, cold, high salt, ABA, heat and UV
). Dark-grown plants" 129 t

BASE COUNT 122 a 105 c 64 g 129 t

ORIGIN

Query Match 66.1%; Score 15.2; DB 10; Length 420;
 Best Local Similarity 47.8%; Pred. No. 2.2e+03;
 Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 CANANCKRAASMANCNRSYTC 23
 ||| 1:||||:| |::|
 Db 170 CAGATCGGACCATCTCGGTTTC 192

RESULT 12
 AV808550 423 bp mRNA linear EST 29-MAR-2002
 LOCUS AV808550 Arabidopsis thaliana cDNA clone RAFL09-55-El5 3',
 DEFINITION mRNA sequence.
 VERSION AV808550
 KEYWORDS AV808550.1 GI:19842535
 SOURCE EST.
 ORGANISM thale cress.
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 423)
 REFERENCE Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
 Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
 Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.,
 and Shinozaki, K.
 Large scale analysis of Arabidopsis full-length cDNA (2002b)
 JOURNAL Unpublished (2002)
 COMMENT Contact: Motoaki Seki

Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060
 Email: mseki@rc.riken.go.jp
 An Arabidopsis full-length cDNA library was constructed essentially
 as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
 and XhoI was ligated to modified lambda phage-1 vector (Carninci et
 al., submitted for publication) digested with BamHI and SalI. This
 clone is in a modified phagescript vector. Please visit our web
 site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
 details.

FEATURES
 source Location/Qualifiers
 1..423
 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"
 /clone="RAFL09-55-El5"
 /clone_1lb="RAFL9"
 /dev_stage="plants at various developmental stages from
 germination to mature seeds"
 /lab_host="DH10B"
 /note="Site_1: BamHI; Site_2: SalI; subjected to
 dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24
 hr) treatments" 121 a 101 c 72 g 129 t

BASE COUNT 121 a 101 c 72 g 129 t

ORIGIN

Query Match 66.1%; Score 15.2; DB 10; Length 423;
 Best Local Similarity 47.8%; Pred. No. 2.2e+03;
 Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 CANANCKRAASMANCNRSYTC 23
 ||| 1:||||:| |::|
 Db 114 CAGATCGGACCATCTCGGTTTC 136

RESULT 13
 A2863097 431 bp DNA linear GSS 21-FEB-2001
 LOCUS A2863097 Mouse 10kb plasmid U06C1M library Mus musculus genomic
 DEFINITION 2M0171003P Mouse 10kb plasmid U06C1M library Mus musculus genomic
 clone U06C2M0171003 F, DNA sequence.
 ACCESSION A2863097
 VERSION A2863097.1 GI:13061059
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 431)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Baecorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0171 row: 0 column: 03
 Seq primer: CCTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 431.
 Location/Qualifiers
 1..431
 /organism="Mus musculus"

```

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U082M0171003"
/clone_lib="Mouse 10kb plasmid U082M0171003"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PMD42nv, purified genomic DNA from Mus musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a C.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1473211419b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT      87 a      143 c      112 g      89 t
ORIGIN

Query Match      66.1% Score 15.2: DB 17: Length 431:
Best Local Similarity 47.8% Pred No. 2.2e+03:
Matches 11: Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY      1 CANANCKRA5MANCCRSYTC 23
Db      372 CAGATGCTGAGAGACCCGCTC 394

RESULT 14
LOCUS B0468428/c
DEFINITION B0468428 HM Hordeum vulgare cDNA clone HM01D16 5-PRIME, mRNA
sequence.
B0468428
B0468428.1 GI:21276210
EST.
SOURCE Hordeum vulgare.
ORGANISM Hordeum vulgare.
Molecular: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
1 (bases 1 to 455)
Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.
EST sequencing and analysis in barley (2002)
Unpublished (2002)
Contact: Stein, N.
Molecular: Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3 06466, Gatersleben, Germany
Tel: 039483-5522
Fax: 039483-5595
Email: stein@ipk-gatersleben.de
Insert Length: 455 Std Error: 0.00
Plate: 1 row: D column: 16
Seq primer: 13.
Location/Qualifiers
1..455
/organism="Hordeum vulgare"
/cultivar="Barke"
/db_xref="taxon:4513"
/clone="HM01D16"
/clone_lib="HM"
/tissue_type="male inflorescences"
/dev_stage="male inflorescences (approx. 2 mm in size),

```

```

green anther stage"
/lab_host="XL10-Gold"
/notes="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream of EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."

BASE COUNT      69 a      138 c      180 g      68 t
ORIGIN

Query Match      66.1% Score 15.2: DB 14: Length 455:
Best Local Similarity 47.8% Pred No. 2.3e+03:
Matches 11: Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY      1 CANANCKRA5MANCCRSYTC 23
Db      287 CAGACCGCGACACCCGCGCTC 265

RESULT 15
LOCUS A2560473/c
DEFINITION A2560473 RPCT-23-180N17.TJ RPCT-23 Mus musculus genomic clone RPCT-23-180N17
, DNA sequence.
A2560473
A2560473.1 GI:11240293
GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
Molecular: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 457)
Zhao, S., Nieman, W., Feldblum, T., Malek, J., Shatsman, S., Akintet,
B., Levins, M., McGann, S., Tesgaye, G., Geer, K., Krol, M., de Jong, P.
and Fraser, C.M.
Mouse BAC End Sequences from Library RPCT-23
Unpublished (1999)
Other GSS: RPCT-23-180N17.TJ
Contact: Shaying Zhao
Department of Pukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCT-23. For BAC
library availability, please contact Pieter de Jong
(pieter@edjong.med.buitalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buitalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 180 row: N column: 17
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
1..457
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCT-23-180N17"
/clone_lib="RPCT-23"
/sex="Female"
/lab_host="DH10B"
/notes="Organ: Kidney/Brain; Vector: pBAC3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBAC3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."

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BASE COUNT 149 a 89 c 85 g 134 t
ORIGIN

Query Match 66.1%; Score 15.2; DB 17; Length 457;
Best Local Similarity 47.8%; Pred. No. 2.3e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CANANNCKRAASMANCCNRSYTC 23
|||::|::|::|::|::|
Db 157 CACATCTAATACCCACCCAGCTC 135

Search completed: March 10, 2003, 06:42:46
Job time : 1341 secs

GenCore version 5.1.4_p5-4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 05:19:34 ; Search time 39.5 Seconds
(without alignments)
178.571 Million cell updates/sec

Title: US-09-975-842-2

Sequence: 1 ggnntccngnttymgntng 23

Scoring table: IDENTITY_NUC
Gapc 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents, NA: *
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4: /cgn2_6/prodata/1/lna/5B.COMB.seq: *
5: /cgn2_6/prodata/1/lna/5A.COMB.seq: *
6: /cgn2_6/prodata/1/lna/5B.COMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.4	67.0	23	1	US-08-724-194-9 Sequence 9, Appli
2	15.4	67.0	23	4	US-09-171-482-5 Sequence 5, Appli
3	15.4	67.0	961	4	US-08-846-826A-3 Sequence 3, Appli
4	15.4	67.0	968	4	US-08-846-826A-1 Sequence 1, Appli
5	15.4	67.0	994	2	US-08-860-577-7 Sequence 7, Appli
6	15.4	67.0	1080	3	US-09-043-627-1 Sequence 1, Appli
7	15.4	67.0	1096	3	US-09-043-627-7 Sequence 7, Appli
8	15.4	67.0	1098	3	US-09-043-627-5 Sequence 5, Appli
9	15.4	67.0	1104	3	US-09-043-627-3 Sequence 3, Appli
10	15.4	67.0	1113	2	US-08-860-577-9 Sequence 9, Appli
11	15.4	67.0	1384	2	US-08-860-577-1 Sequence 1, Appli
12	15.4	67.0	1703	1	US-07-809-457A-8 Sequence 8, Appli
13	15.4	67.0	1800	1	US-08-553-943-8 Sequence 8, Appli
14	15.4	67.0	1800	1	PCT-US91-09437-8 Sequence 8, Appli
15	15.4	67.0	1878	1	US-08-724-194-3 Sequence 3, Appli
16	15.4	67.0	1888	1	US-08-485-107-1 Sequence 1, Appli
17	15.4	67.0	2040	2	US-08-869-412B-11 Sequence 11, Appli
18	15.4	67.0	2040	4	US-09-255-154D-11 Sequence 11, Appli
19	15.4	67.0	2230	4	US-08-578-313-24 Sequence 24, Appli
20	15.4	67.0	4459	2	US-09-363-243-2 Sequence 2, Appli
21	15.4	67.0	5613	2	US-08-463-418-1 Sequence 1, Appli
22	15.4	67.0	7244	4	US-08-378-313-26 Sequence 26, Appli
23	15.4	67.0	7587	4	US-08-378-313-22 Sequence 22, Appli
24	15.4	67.0	9060	4	US-08-378-313-20 Sequence 20, Appli
25	15.4	67.0	15397	2	US-08-673-768-1 Sequence 1, Appli
26	15.4	67.0	15397	2	US-08-673-768-1 Sequence 1, Appli
27	15.4	67.0	15397	2	US-08-673-768-1 Sequence 1, Appli

28	14.4	62.6	70	4	US-09-364-380-27 Sequence 27, Appli
29	14.4	62.6	1155	2	US-08-331-644-4 Sequence 4, Appli
30	14.4	62.6	1155	5	PCT-US93-04102-4 Sequence 4, Appli
31	14.2	61.7	90	4	US-08-464-700-40 Sequence 40, Appli
32	14.2	61.7	92	4	US-08-464-700-15 Sequence 15, Appli
33	14.2	61.7	1497	2	US-08-860-577-11 Sequence 11, Appli
34	14.2	61.7	1712	2	US-08-632-598-1 Sequence 1, Appli
35	14.2	61.7	1712	4	US-09-231-240-1 Sequence 1, Appli
36	14.2	61.7	1945	1	US-08-724-194-1 Sequence 1, Appli
37	14.2	61.7	2210	4	US-08-464-700-53 Sequence 53, Appli
38	14.2	61.7	2210	4	US-08-464-700-37 Sequence 37, Appli
39	14.2	61.7	2427	2	US-08-678-039A-39 Sequence 39, Appli
40	14.2	61.7	2678	2	US-08-724-194-7 Sequence 7, Appli
41	14.2	61.7	246240	1	US-08-724-194A-20 Sequence 20, Appli
42	14.2	61.7	246240	2	US-08-724-194A-21 Sequence 21, Appli
43	14.2	61.7	246240	2	US-08-724-194A-22 Sequence 22, Appli
44	14.2	61.7	246240	2	US-08-724-194A-22 Sequence 22, Appli
45	13.8	60.0	238	1	US-07-903-466-32 Sequence 32, Appli

ALIGNMENTS

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RESULT 1
US-08-724-194-9
: Sequence 9, Application US/08724194
: Patent No. 5824875
: GENERAL INFORMATION:
: APPLICANT: RAND, RAJINDER S.
: TITLE OF INVENTION: ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE
: TITLE OF INVENTION: SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS
: NUMBER OF INVENTIONS: 13
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: SANTANGELO LAW OFFICES PC
: STREET: 315 WEST OAK STREET, STE 701
: CITY: FORT COLLINS
: STATE: CO
: COUNTRY: USA
: ZIP: 80521
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/724,194
: FILING DATE: 01-OCT-1996
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: SANTANGELO, LUKE
: REGISTRATION NUMBER: 31,997
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (970) 224-3100
: INFORMATION FOR SEQ ID NO:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 23 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: misc-feature
: LOCATION: group(3, 6, 9, 12, 18, 21)
: OTHER INFORMATION: /note="N represents inosine"
US-08-724-194-9
Query Match 67.0%; Score 15.4; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGTNCNGGNTTYMGNTNG 23
DB 1 GGGTNCNGGNTTYMGNTNG 23

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RESULT 2
US-09-171-482-5
Sequence 5, Application US/09171482A
Patent No. 6184449
GENERAL INFORMATION:
APPLICANT: Ranu, Rajinder S.
TITLE OF INVENTION: A 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE GENE FROM
FILE REFERENCE: TAGAWA-ROSE
CURRENT FILING DATE: 1998-10-19
EARLIER APPLICATION NUMBER: PCT/US97/17644, Published under WO98/14465; US5,824,875
EARLIER FILING DATE: 1997-Sept-30, Published 1998-April-09; 1996-Oct-01
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Word Perfect 6.1
SEQ ID NO: 5
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: 1
LOCATION: 3, 6, 9, 12, 18, and 21
OTHER INFORMATION: PCR primer
US-09-171-482-5

Query Match 67.0%; Score 15.4; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGNATCCGNGNTTYGNTNGC 23
DB 1 GGNATCCGNGNTTYGNTNGC 23

RESULT 3
US-08-846-826A-3
Sequence 3, Application US/08846826A
Patent No. 6194639
GENERAL INFORMATION:
APPLICANT: Botella, Jose
APPLICANT: Sanewski, Garth
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES FROM PINEAPPLES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: One Commerce Square, 2005 Market Street, 22nd
STREET: Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103-7086
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,826A
FILING DATE: 01-MAY-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN9582
FILING DATE: 01-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Nadel Esq., Alan S.
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1280
TELEFAX: 215-567-2991
TELEX: 831-494

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 961 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..102
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 103..194
FEATURE:
NAME/KEY: CDS
LOCATION: 195..961
US-08-846-826A-3

Query Match 67.0%; Score 15.4; DB 4; Length 961;
Best Local Similarity 56.5%; Pred. No. 18;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGNATCCGNGNTTYGNTNGC 23
DB 567 GGCTACACAGCTTCGCGTCGG 589

RESULT 4
US-08-846-826A-1
Sequence 1, Application US/08846826A
Patent No. 6194639
GENERAL INFORMATION:
APPLICANT: Botella, Jose
APPLICANT: Sanewski, Garth
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES FROM PINEAPPLES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: One Commerce Square, 2005 Market Street, 22nd
STREET: Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103-7086
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,826A
FILING DATE: 01-MAY-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN9582
FILING DATE: 01-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Nadel Esq., Alan S.
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1280
TELEFAX: 215-567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 968 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS

Page 3

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/043,627
FILING DATE: 20-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU96/00591
FILING DATE: 20-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN5559
FILING DATE: 20-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN9603
FILING DATE: 02-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bernstein, Scott N.
REGISTRATION NUMBER: 38,827
REFERENCE/DOCKET NUMBER: 3573-11US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-924-8555
TELEFAX: 609-924-3036
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1096 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1095
US-09-043-627-7

Query Match          67.0%; Score 15.4; DB 3; Length 1096;
Best Local Similarity 56.5%; Pred. No. 18;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNATNCNGMNTYMGNTNG 23
DB 688 GGCTCTCCCGGTTTCCGGGTAGG 710

RESULT 8
US-09-043-627-5
Sequence 3, Application US/09043627
Patent No. 6124525
GENERAL INFORMATION:
APPLICANT: Botella, Jose Ramon
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
STREET: 100 Thanel Circle, Suite 306
CITY: Princeton
STATE: NJ
COUNTRY: USA
ZIP: 08540-3662
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/043,627
FILING DATE: 20-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU96/00591
FILING DATE: 20-SEP-1996
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN5559
FILING DATE: 20-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN9603
FILING DATE: 02-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bernstein, Scott N.
REGISTRATION NUMBER: 38,827
REFERENCE/DOCKET NUMBER: 3573-11US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-924-8555
TELEFAX: 609-924-3036
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1098
US-09-043-627-5

Query Match          67.0%; Score 15.4; DB 3; Length 1098;
Best Local Similarity 56.5%; Pred. No. 18;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNATNCNGMNTYMGNTNG 23
DB 688 GGCTCTCCCGGTTTCCGGGTAGG 710

RESULT 9
US-09-043-627-3
Sequence 3, Application US/09043627
Patent No. 6124525
GENERAL INFORMATION:
APPLICANT: Botella, Jose Ramon
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
STREET: 100 Thanel Circle, Suite 306
CITY: Princeton
STATE: NJ
COUNTRY: USA
ZIP: 08540-3662
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/043,627
FILING DATE: 20-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU96/00591
FILING DATE: 20-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN5559
FILING DATE: 20-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN9603
FILING DATE: 02-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bernstein, Scott N.
REGISTRATION NUMBER: 38,827
REFERENCE/DOCKET NUMBER: 3573-11US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-924-8555
```

TELEFAX: 609-924-3036
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1104
US-09-043-627-3

Query Match
Best Local Similarity 56.5%; Pred. No. 18;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGNATCCGCGATTAGAGTTGG 719
DB 697 GGATTCCTCGATTAGAGTTGG 719

RESULT 10
US-09-043-627-9
Sequence 9, Application US/09043627
Patent No. 6124525
GENERAL INFORMATION:
APPLICANT: Botella, Jose Ramon
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
STREET: 100 Thane Circle, Suite 306
CITY: Princeton
STATE: NJ
COUNTRY: USA
ZIP: 08540-3662
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/043,627
FILING DATE: 20-MAR-1998
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/AU96/00591
FILING DATE: 23-SEP-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: AU P95559
FILING DATE: 23-SEP-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: AU P96603
FILING DATE: 02-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bernsclahn, Scott N
REGISTRATION NUMBER: 38,827
REFERENCE/DOCKET NUMBER: 3573-11US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-924-8555
TELEFAX: 609-924-3036
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1113 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1113
US-09-043-627-9

Query Match
Best Local Similarity 56.5%; Pred. No. 18;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGNATCCGCGATTAGAGTTGG 719
DB 694 GCGTCCGCGATTAGAGTTGG 716

RESULT 11
US-08-860-577-1
Sequence 1, Application US/08860577
Patent No. 5998702
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L.
APPLICANT: Deng, Rosaline Z.
APPLICANT: Carney, Kim J.
APPLICANT: Rutencutter, Glen E.
APPLICANT: Reynolds, John F.
TITLE OF INVENTION: Transgenic Plants Expressing ACC
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamov & Katz, Ltd
STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
STREET: 4700
CITY: Chicago
STATE: IL
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,577
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V.
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1384 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 2..39
FEATURE:
NAME/KEY: CDS
LOCATION: 135..433
FEATURE:
NAME/KEY: CDS
LOCATION: 595..1383
US-08-860-577-1

Query Match
Best Local Similarity 56.5%; Pred. No. 19;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGNATCCGCGATTAGAGTTGG 23
DB 970 GGTCTCCGCGATTAGAGTTGG 992

RESULT 12
US-08-378-313-18
Sequence 18, Application US/08378313
Patent No. 6207881
GENERAL INFORMATION:
APPLICANT: THEOLOGIS, ATHANASIOS
TITLE OF INVENTION: SATO, TAKAHITO
TITLE OF INVENTION: GENETIC CONTROL OF FRUIT RIPENING THROUGH
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,313
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,493
FILING DATE: 02-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29190-20002.20
TELEPHONE: (415) 856-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ. ID NO.: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1703 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 11..1489
US-08-378-313-18
Query Match 67.0%; Score 15.4; DB 4; Length 1703;
Best Local Similarity 56.5%; Pred. No. 20;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 GGNATCCGNGNTTYMGNTNGC 23
DB 854 GGCCTCCGCTGCTTCGAGTGG 876
RESULT 13
US-07-809-457A-8
Sequence 8, Application US/07809457A
Patent No. 5512466
GENERAL INFORMATION:
APPLICANT: Kiese, Harry J.
APPLICANT: Kishore, Ganesh M.
TITLE OF INVENTION: Control of Fruit Ripening and Senescence
TITLE OF INVENTION: In Plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Monsanto Co. BBAF
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri

COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/809,457A
FILING DATE: 19911217
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,440
FILING DATE: 26-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10538)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ. ID NO.: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1800 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
US-07-809-457A-8
Query Match 67.0%; Score 15.4; DB 1; Length 1800;
Best Local Similarity 56.5%; Pred. No. 20;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 GGNATCCGNGNTTYMGNTNGC 23
DB 994 GGGTACGAGATTAGAGTGG 1016
RESULT 14
US-08-553-943-8
Sequence 8, Application US/08553943
Patent No. 5702933
GENERAL INFORMATION:
APPLICANT: Kiese, Harry J.
APPLICANT: Kishore, Ganesh M.
TITLE OF INVENTION: Control of Fruit Ripening and Senescence
TITLE OF INVENTION: In Plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Monsanto Co. BBAF
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,943
FILING DATE: 06-NOV-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/809,457
FILING DATE: 17-DEC-1991
APPLICATION NUMBER: US 07/632,440
FILING DATE: 26-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914

REFERENCE/DOCKET NUMBER: 38-21(10538)A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314)537-6099
 TELEFAX: (314)537-6047
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1800 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 US-08-553-943-8

Query Match
 Best Local Similarity 67.0%; Score 15.4; DB 1; Length 1800;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNATCCGCGATTTAGATCGG 23
 Db 994 GGGTACCGAGATTAGATCGG 1016

RESULT 15
 PCT-US91-09437-8
 Sequence 8, Application PC/TUS9109437
 GENERAL INFORMATION:
 APPLICANT: Kiehl, Harry J.
 APPLICANT: Kistore, Ganesh M.
 TITLE OF INVENTION: Control of Fruit Ripening and Senescence
 TITLE OF INVENTION: In Plants
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Monsanto Co. BBAF
 STREET: 700 Chesterfield Village Parkway
 CITY: St. Louis
 STATE: Missouri
 COUNTRY: USA
 ZIP: 63198
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US91/09437
 FILING DATE: 19911217
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/632,440
 FILING DATE: 26-DEC-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Hoerner, Jr., Dennis R.
 REGISTRATION NUMBER: 30,914
 REFERENCE/DOCKET NUMBER: 38-21(10538)A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314)537-6099
 TELEFAX: (314)537-6047
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1800 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 PCT-US91-09437-8

Query Match
 Best Local Similarity 67.0%; Score 15.4; DB 5; Length 1800;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 OY 1 GGNATCCGCGATTTAGATCGG 23
 Db 994 GGGTACCGAGATTAGATCGG 1016

GenCore version 5.1.4-p5-4578
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 05:19:34 ; Search time 39.5 Seconds
(without alignments)
178.571 Million cell updates/sec

Title: US-09-975-842-3

Sequence: 1 cananckraasmanccnrsytc 23

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2-6/ptcdat1/1na/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	15.2	66.1	23	1	US-08-724-194-10
2	15.2	66.1	23	4	US-09-171-482-6
3	15.2	66.1	1096	3	US-09-043-627-7
4	15.2	66.1	1098	3	US-09-043-627-5
5	15.2	66.1	1104	3	US-09-043-627-3
6	15.2	66.1	1703	4	US-08-378-313-18
7	15.2	66.1	1712	2	US-08-632-598-1
8	15.2	66.1	1712	4	US-09-231-240-1
9	15.2	66.1	1743	4	US-09-171-482-1
10	15.2	66.1	1800	1	US-07-809-457A8
11	15.2	66.1	1800	1	US-08-553-94378
12	15.2	66.1	1800	5	PCT-US91-09437-8
13	15.2	66.1	1878	1	US-08-724-194-3
14	15.2	66.1	1888	1	US-08-483-107-1
15	15.2	66.1	1945	1	US-08-724-194-11
16	15.2	66.1	2040	2	US-08-695-412B-11
17	15.2	66.1	2040	4	US-09-253-134D-11
18	15.2	66.1	2230	4	US-08-378-313-24
19	15.2	66.1	2678	1	US-08-724-194-2
20	15.2	66.1	2613	1	US-08-463-418-1
21	15.2	66.1	7244	4	US-08-378-313-26
22	15.2	66.1	7587	4	US-08-378-313-22
23	15.2	66.1	9060	4	US-08-673-768-1
24	15.2	66.1	13397	2	US-08-673-768-1
25	15.2	66.1	13397	2	US-08-673-768-1
26	15.2	61.7	1497	2	US-08-860-577-11
27	14	60.9	4712	4	US-09-221-017B-577

C 28	14	60.9	11613	1	US-08-484-044-10	Sequence 10, Appl
C 29	13.6	59.1	720	3	US-09-306-881-3	Sequence 3, Appl
C 30	13.6	59.1	1200	4	US-09-327-681-5	Sequence 5, Appl
C 31	13.6	59.1	2832	4	US-09-397-885-6	Sequence 6, Appl
C 32	13.6	59.1	3033	1	US-08-453-695A-111	Sequence 11, App
C 33	13.6	59.1	3033	1	US-08-268-161A-111	Sequence 11, App
C 34	13.6	59.1	3033	2	US-08-453-702A-111	Sequence 11, App
C 35	13.6	59.1	3033	4	US-09-099-639-111	Sequence 11, App
C 36	13.6	59.1	3033	5	PCT-US95-08071-111	Sequence 11, App
C 37	13.6	59.1	4459	4	US-09-363-243-2	Sequence 2, Appl
C 38	13.6	59.1	4791	4	US-08-949-155-49	Sequence 49, Appl
C 39	13.6	59.1	4791	4	US-09-819-964-49	Sequence 49, Appl
C 40	13.6	59.1	10504	4	US-09-423-744A-19	Sequence 19, Appl
C 41	13.6	59.1	12143	4	US-09-423-744A-19	Sequence 1, Appl
C 42	13.2	57.4	20	3	US-09-043-627-15	Sequence 15, Appl
C 43	13.2	57.4	961	4	US-08-846-826A-3	Sequence 3, Appl
C 44	13.2	57.4	966	4	US-08-846-826A-3	Sequence 1, Appl
C 45	13.2	57.4	998	1	US-08-553-516-1	Sequence 1, Appl

ALIGNMENTS

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RESULT 1
US-08-724-194-10
Sequence 10, Application US/08724194
Patent No. 5824875
GENERAL INFORMATION:
APPLICANT: RANU, RAJINDER S.
TITLE OF INVENTION: ONE-AMINOACIDOPROBANE-1-CARBOXYLATE
TITLE OF INVENTION: SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS
NUMBER OF INVENTIONS: 13
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSES:
ADDRESS: SANTANGELO LAW OFFICES PC
STREET: 315 WEST OAK STREET, STE 701
CITY: FORT COLLINS
STATE: CO
COUNTRY: USA
ZIP: 80521
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,194
CLASSIFICATION: 800
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: SANTANGELO, LUKR
REGISTRATION NUMBER: 31,997
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 224-3100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: misc.feature
LOCATION: group(3, 5, 6, 15, 18)
OTHER INFORMATION: /note="N represents Inosine"
US-08-724-194-10
Query Match 66.1%; Score 15.2; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CANANCKRAASMANCCNRSYTC 23
Db 1 CANANCKRAASMANCCNRSYTC 23

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? INFORMATION FOR SEQ ID NO: 5
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? SEQUENCE CHARACTERISTICS:
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?   LENGTH: 1098 base pairs
?   TYPE: nucleic acid
?   STRANDEDNESS: single
?   TOPOLOGY: linear
?
?   MOLECULE TYPE: cDNA
?
?   FEATURE:
?
?   NAME/KEY: CDS

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LOCATION: 1.1098
US-09-043-627-5
Query Match
Best Local Similarity 66.1%; Score 15.2; DB 3; Length 1098;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CANANCKRASAAMCNCNRSYTC 23
DB 1091 CAACTCTGACACCCCGGCTC 1069

RESULT 5
US-09-043-627-3/c
Sequence 3, Application US/09043627
Patent No. 6124525
GENERAL INFORMATION:
APPLICANT: Botella, Jose Ramon
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
STREET: 100 Thanel Circle, Suite 306
CITY: Princeton
STATE: NJ
COUNTRY: USA
ZIP: 08540-3662
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 20-MAR-1998
APPLICATION NUMBER: US/09/043,627
CLASSIFICATION: 800
PRIORITY INFORMATION:
PRIORITY APPLICATION DATA:
PCT/AU96/00591
FILING DATE: 20-SEP-1996
APPLICATION NUMBER: AU PN5559
FILING DATE: 20-SEP-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: AU PN9603
FILING DATE: 02-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bernstein, Scott N
REGISTRATION NUMBER: 38,827
REFERENCE/DOCKET NUMBER: 3573-11US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-924-8555
TELEFAX: 609-924-3036
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1104
US-09-043-627-3

Query Match
Best Local Similarity 66.1%; Score 15.2; DB 3; Length 1104;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CANANCKRASAAMCNCNRSYTC 23
DB 1097 CAGACCGTGAACGACCGAGTTC 1075
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RESULT 6
US-08-378-313-18/c
Sequence 18, Application US/08378313
Patent No. 6207881
GENERAL INFORMATION:
APPLICANT: THEOLOGIS, ATHANASIOS
APPLICANT: SATO, TAKAHIDO
TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,313
FILING DATE:
CLASSIFICATION: 800
PRIORITY INFORMATION:
PRIORITY APPLICATION DATA:
US 07/862,493
FILING DATE: 02-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29190-20002.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 856-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1703 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1703
US-08-378-313-18

Query Match
Best Local Similarity 66.1%; Score 15.2; DB 4; Length 1703;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CANANCKRASAAMCNCNRSYTC 23
DB 1254 CAAACTCGAAACCAACCTGCTC 1232

RESULT 7
US-08-632-598-1/c
Sequence 1, Application US/08632598
Patent No. 5886164
GENERAL INFORMATION:
APPLICANT: BIRD, COLIN R
APPLICANT: PIETCHER, JONATHAN D
TITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY AND CUSHMAN
STREET: 100 NEW YORK AVENUE N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,598
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 223355/SEE50112/US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 861-3000
TELEFAX: 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1712 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: MUSA
IMMEDIATE SOURCE:
CLONE: ACS GENE
US-08-632-598-1

Query Match 66.1%; Score 15.2; DB 2; Length 1712;
Best Local Similarity 47.8%; Pred. No. 43;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CANANCKRASMNCNRSYTC 23
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Db 1265 CACACCTGAACACCCCGGCTC 1243

RESULT 8
US-09-231-240-1/c
Sequence 1, Application US/09231240
Patent No. 6262346
GENERAL INFORMATION:
APPLICANT: BIRD, COLIN R
APPLICANT: FLETCHER, JONATHON D
TITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARY AND CUSHMAN
STREET: 1100 NEW YORK AVENUE N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,240
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,598
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 223355/SEE50112/US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 861-3000
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TELEFAX: 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1712 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: MUSA
IMMEDIATE SOURCE:
CLONE: ACS GENE
US-09-231-240-1

Query Match 66.1%; Score 15.2; DB 4; Length 1712;
Best Local Similarity 47.8%; Pred. No. 43;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CANANCKRASMNCNRSYTC 23
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Db 1265 CACACCTGAACACCCCGGCTC 1243

RESULT 9
US-09-171-482-1/c
Sequence 1, Application US/09171482A
Patent No. 618449
GENERAL INFORMATION:
APPLICANT: Ranu, Rajinder S.
TITLE OF INVENTION: A 1-MINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE GENE FROM
FILE REFERENCE: TAGANA-ROSE
CURRENT FILING DATE: 1998-10-19
EARLIER APPLICATION NUMBER: PCT/US97/17644, Published under W098/14465; US5,824,87
EARLIER FILING DATE: 1997-Sept-30, Published 1998-April-09; 1996-Oct-01
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Word Perfect 6.1
SEQ ID NO 1
LENGTH: 1743
TYPE: DNA
ORGANISM: Rosa kardinal
US-09-171-482-1

Query Match 66.1%; Score 15.2; DB 4; Length 1743;
Best Local Similarity 47.8%; Pred. No. 43;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CANANCKRASMNCNRSYTC 23
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Db 1628 CAAACCGGACCAATCCCGTTC 1606

RESULT 10
US-07-809-457A-8/c
Sequence 8, Application US/07809457A
Patent No. 5512466
GENERAL INFORMATION:
APPLICANT: Klee, Harry J.
APPLICANT: Kishore, Ganesh M.
TITLE OF INVENTION: Control of Fruit Ripening and Senescence
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Monsanto Co. B84F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/07/809,457A
  FILING DATE: 19911217
  CLASSIFICATION: 800
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 07/632,440
    FILING DATE: 26-DEC-1990
  ATTORNEY/AGENT INFORMATION:
    NAME: Hoerner Jr., Dennis R.
    REGISTRATION NUMBER: 30,914
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (314)537-6099
      TELEFAX: (314)537-6047
  INFORMATION FOR SEQ ID NO: 8:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 1800 base pairs
      TYPE: NUCLEIC ACID
      STRANDEDNESS: double
      TOPOLOGY: linear
    MOLECULE TYPE: cDNA to mRNA
  US-07-809-457A-8

Query Match
Best Local Similarity 47.8%; DB 1; Length 1800;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CANANCKRA$AMCNCRSYTC 23
Db 1394 CAAACTCGAGACACCGTGCTC 1372

RESULT 11
US-08-553-943-8/c
Sequence 8, Application US/08553943
Patent No. 570293
GENERAL INFORMATION:
  APPLICANT: Klee, Harry J.
  TITLE OF INVENTION: Control of Fruit Ripening and Senescence
  NUMBER OF SEQUENCES: 17
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Monsanto Co., BBAF
    STREET: 700 Chesterfield Village Parkway
    CITY: St. Louis
    STATE: Missouri
    COUNTRY: USA
  ZIP: 63198
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/553,943
    FILING DATE: 06-NOV-1995
  CLASSIFICATION: 800
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 07/809,457
    FILING DATE: 17-DEC-1991
    APPLICATION NUMBER: US 07/632,440
    FILING DATE: 26-DEC-1990
  ATTORNEY/AGENT INFORMATION:
    NAME: Hoerner Jr., Dennis R.
    REGISTRATION NUMBER: 30,914
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (314)537-6099
      TELEFAX: (314)537-6047
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
  LENGTH: 1800 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: double
  TOPOLOGY: linear
  MOLECULE TYPE: cDNA to mRNA
  US-08-553-943-8

Query Match
Best Local Similarity 47.8%; DB 1; Length 1800;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CANANCKRA$AMCNCRSYTC 23
Db 1394 CAAACTCGAGACACCGTGCTC 1372

RESULT 12
PCT-US91-09437-8/c
Sequence 8, Application PC/TUS9109437
GENERAL INFORMATION:
  APPLICANT: Klee, Harry J.
  TITLE OF INVENTION: Control of Fruit Ripening and Senescence
  NUMBER OF SEQUENCES: 17
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Monsanto Co., BBAF
    STREET: 700 Chesterfield Village Parkway
    CITY: St. Louis
    STATE: Missouri
    COUNTRY: USA
  ZIP: 63198
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: PCT/US91/09437
    FILING DATE: 19911217
  CLASSIFICATION: 800
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 07/632,440
    FILING DATE: 26-DEC-1990
  ATTORNEY/AGENT INFORMATION:
    NAME: Hoerner Jr., Dennis R.
    REGISTRATION NUMBER: 30,914
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (314)537-6099
      TELEFAX: (314)537-6047
  INFORMATION FOR SEQ ID NO: 8:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 1800 base pairs
      TYPE: NUCLEIC ACID
      STRANDEDNESS: double
      TOPOLOGY: linear
    MOLECULE TYPE: cDNA to mRNA
  PCT-US91-09437-8

Query Match
Best Local Similarity 47.8%; DB 5; Length 1800;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CANANCKRA$AMCNCRSYTC 23
Db 1394 CAAACTCGAGACACCGTGCTC 1372

RESULT 13
US-08-724-194-3/c
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Mon Mar 10 03:10:49 2003

us-09-975-842-3.mli

Page 7

Db 1315 CAAACCTAAGCACCOCGGCTC 1293

Search completed: Merch 10, 2003, 06:44:21
Job time : 44 secs

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 05:25:27 ; Search time 50.5 Seconds
(without alignments)
304.201 Million cell updates/sec

Title: US-C9-975-842-2
Perfect score: 23
Sequence: 1 ggnntcngngnttymgrrtng 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 478924 seqs, 333959956 residues

Total number of hits satisfying chosen parameters: 957848

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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3: /cgn2_6/ptodata1/pubna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata1/pubna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata1/pubna/US07_NEW_PUB.seq:*
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12: /cgn2_6/ptodata1/pubna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata1/pubna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata1/pubna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	15.4	67.0	23	US-09-776-529A-5	Sequence 5, Appl1
2	15.4	67.0	748	US-09-770-149-16	Sequence 16, Appl1
3	15.4	67.0	1344	US-09-938-842A-1571	Sequence 1571, Ap
4	14.4	62.6	274	US-09-294-093B-4729	Sequence 4729, Ap
5	14.4	62.6	1506	US-09-963-285-9	Sequence 9, Appl1
6	14.4	62.6	2712	US-09-963-285-6	Sequence 6, Appl1
7	14.4	62.6	3289	US-09-963-285-8	Sequence 8, Appl1
8	14.4	62.6	4158	US-09-963-285-3	Sequence 3, Appl1
9	14.4	62.6	6021	US-09-963-285-5	Sequence 5, Appl1
10	14.4	62.6	6458	US-09-963-285-1	Sequence 1, Appl1
11	14.2	61.7	536	US-09-974-879-57	Sequence 57, Appl1
12	14.2	61.7	1488	US-09-938-842A-1726	Sequence 1726, Ap
13	14.2	61.7	2099	US-09-822-830A-14	Sequence 14, Appl1
14	14.2	61.7	2242	US-09-954-456-542	Sequence 542, Ap
15	14.2	61.7	2274	US-09-921-771-5	Sequence 5, Appl1
16	14.2	61.7	14962	US-09-764-878-244	Sequence 244, Ap
17	14.2	61.7	15849	US-09-880-107-362	Sequence 2362, Ap
18	13.8	60.0	363	US-09-864-761-24268	Sequence 24268, Ap
19	13.8	60.0	421	US-09-925-299-409	Sequence 409, Ap

C 20	13.8	60.0	421	10	US-09-925-299-409	Sequence 409, App
C 21	13.8	60.0	574	10	US-09-864-761-13696	Sequence 13696, A
C 22	13.8	60.0	594	10	US-09-864-761-7563	Sequence 7563, Ap
C 23	13.8	60.0	3015	9	US-10-161-510-6	Sequence 6, Appl1
C 24	13.8	60.0	22161	10	US-09-764-847-1020	Sequence 1020, Ap
C 25	13.8	60.0	110096	10	US-09-880-107-1542	Sequence 1542, Ap
C 26	13.4	58.3	308	10	US-09-867-701-3531	Sequence 3531, Ap
C 27	13.4	58.3	451	10	US-09-876-889-320	Sequence 320, App
C 28	13.4	58.3	609	10	US-09-833-381-925	Sequence 925, App
C 29	13.4	58.3	813	10	US-09-974-300-293	Sequence 293, App
C 30	13.4	58.3	1743	10	US-09-776-529A-1	Sequence 1, Appl1
C 31	13.4	58.3	1985	10	US-09-880-107-3442	Sequence 3442, App
C 32	13.4	58.3	2093	12	US-10-044-090-292	Sequence 292, App
C 33	13.4	58.3	4485	9	US-10-002-974-1	Sequence 1, Appl1
C 34	13.4	58.3	4485	12	US-10-014-269-33	Sequence 33, Appl1
C 35	13.4	58.3	4486	9	US-10-014-269-33	Sequence 33, Appl1
C 36	13.4	58.3	4486	12	US-10-014-269-33	Sequence 33, Appl1
C 37	13.4	58.3	23626	10	US-09-764-878-261	Sequence 261, App
C 38	13.4	58.3	23626	10	US-09-764-878-261	Sequence 261, App
C 39	13.4	58.3	23632	10	US-09-764-878-262	Sequence 262, App
C 40	13.4	58.3	23632	10	US-09-764-878-262	Sequence 262, App
C 41	13.4	58.3	172637	10	US-09-805-458A-3	Sequence 3, Appl1
C 42	13.2	57.4	375	10	US-09-783-590-10488	Sequence 10488, A
C 43	13.2	57.4	1122	9	US-10-060-432-18	Sequence 18, Appl1
C 44	13.2	57.4	1122	10	US-10-905-173-18	Sequence 18, Appl1
C 45	13.2	57.4	1374	9	US-09-738-626-186	Sequence 186, App

ALIGNMENTS

RESULT 1
US-09-776-529A-5
Sequence 5, Application US/09776529A
Patent No. US20020083484A1
GENERAL INFORMATION:
APPLICANT: Tagawa Greenhouses, Inc.
TITLE OF INVENTION: A 1-Aminocyclopropane-1-Carboxylate Synthase Gene From Rosa to
FILE REFERENCE: Tagawa-Rose
CURRENT APPLICATION NUMBER: US/09/776,529A
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 08/724,194
PRIOR FILING DATE: 1996-10-01
PRIOR APPLICATION NUMBER: US 09/171,482
PRIOR FILING DATE: 1998-10-19
PRIOR APPLICATION NUMBER: PCT/US97/17644
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc-feature
LOCATION: (3), (6), (9), (12), (18), and (21)
OTHER INFORMATION: n=1
US-09-776-529A-5
Query Match 67.0%; Score 15.4; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Ox 1 GGNNTCCNGNTTGMGRRNG 23
Db 1 GGNNTCCNGNTTGMGRRNG 23
RESULT 2
US-09-770-149-16/c

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; Sequence 16, Application US/09770149
; Patent No. US2002005963A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matheev, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krieker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurdan, Patrick
; TITLE OF INVENTION: Expressed sequences of Arabidopsis
; FILE REFERENCE: 2024 (PARA-013PRV)
; CURRENT APPLICATION NUMBER: US/09/770,149
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,506
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 748
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(748)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-149-16

Query Match          67.0%; Score 15.4; DB 10; Length 748;
Best Local Similarity 56.5%; Pred. No. 40;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      1 GGNYNCCGNGNTTYMGNRTNG 23
Db      617 GGTCTTCTGCTGTTTCCGCGTGG 595

RESULT 3
US-09-938-842A-1571
; Sequence 1571, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME. AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1571
; LENGTH: 1344
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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1571

Query Match          67.0%; Score 15.4; DB 9; Length 1344;
Best Local Similarity 56.5%; Pred. No. 44;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      1 GGNYNCCGNGNTTYMGNRTNG 23
Db      862 GGTCTTCTGCTGTTTCCGCGTGG 884

RESULT 4
US-09-294-093B-4729/C
; Sequence 4729, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 4729
; LENGTH: 274
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incycle ID No. US20010051335A1 700354878H1
; LOCATION: 146, 203, 223
; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-4729

Query Match          62.6%; Score 14.4; DB 10; Length 274;
Best Local Similarity 54.5%; Pred. No. 1.2e+02;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      2 GNYTNCNGNGNTTYMGNRTNG 23
Db      60 GTTCCAGGCTTCAGCATGG 39

RESULT 5
US-09-963-285-9
; Sequence 9, Application US/09963285
; Patent No. US20020090707A1
; GENERAL INFORMATION:
; APPLICANT: Enerbäck, Sven
; APPLICANT: Krook, Katarina
; APPLICANT: Rondahl, Lena
; APPLICANT: Wasserman, Wyeth
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-042001
; CURRENT APPLICATION NUMBER: US/09/963,285
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: SE 0004102-0
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/238,897
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: SE 0003435-5
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1506
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1503)
US-09-963-285-9

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Query Match          62.6%; Score 14.4; DB 10; Length 1506;
Best Local Similarity 54.5%; Pred. No. 1.5e+02;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

```

```

QY      1 GGNNTCCNGGNTTYMGRTNG 22
      ||:|||||:|:|:|:|:|:|
Db      796 GGGCTGCCCTGGCTTCACGCTGG 817

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```

RESULT 6
US-09-963-285-6
; Sequence 6, Application US/09963285
; Patent No. US20020090707A1
; GENERAL INFORMATION:
; APPLICANT: Enerbck, Sven
; APPLICANT: Kirook, Katarina
; APPLICANT: Ron Dahl, Lena
; APPLICANT: Wasserman, Wyeth
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-042001
; CURRENT APPLICATION NUMBER: US/09/963,285
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: SE 0004102-0
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/238,897
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: SE 0003435-5
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2712
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (422)...(1903)
US-09-963-285-6

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Query Match          62.6%; Score 14.4; DB 10; Length 2712;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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```

QY      1 GGNNTCCNGGNTTYMGRTNG 22
      ||:|||||:|:|:|:|:|:|
Db      1214 GGGCTGCCCTGGCTTCACGCTGG 1235

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RESULT 7
US-09-963-285-8
; Sequence 8, Application US/09963285
; Patent No. US20020090707A1
; GENERAL INFORMATION:
; APPLICANT: Enerbck, Sven
; APPLICANT: Kirook, Katarina
; APPLICANT: Ron Dahl, Lena
; APPLICANT: Wasserman, Wyeth
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-042001
; CURRENT APPLICATION NUMBER: US/09/963,285
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: SE 0004102-0
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/238,897
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: SE 0003435-5

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; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 3289
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-963-285-8

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Query Match          62.6%; Score 14.4; DB 10; Length 3289;
Best Local Similarity 54.5%; Pred. No. 1.7e+02;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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```

QY      1 GGNNTCCNGGNTTYMGRTNG 22
      ||:|||||:|:|:|:|:|:|
Db      1992 GGGCTGCCCTGGCTTCACGCTGG 2013

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RESULT 8
US-09-963-285-3
; Sequence 3, Application US/09963285
; Patent No. US20020090707A1
; GENERAL INFORMATION:
; APPLICANT: Enerbck, Sven
; APPLICANT: Kirook, Katarina
; APPLICANT: Ron Dahl, Lena
; APPLICANT: Wasserman, Wyeth
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-042001
; CURRENT APPLICATION NUMBER: US/09/963,285
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: SE 0004102-0
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/238,897
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: SE 0003435-5
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4158
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (187)...(1437)
US-09-963-285-3

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Query Match          62.6%; Score 14.4; DB 10; Length 4158;
Best Local Similarity 54.5%; Pred. No. 1.7e+02;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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```

QY      1 GGNNTCCNGGNTTYMGRTNG 22
      ||:|||||:|:~|:|:|:|:|
Db      730 GGGCTGCCCTGGCTTCACGCTGG 751

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RESULT 9
US-09-963-285-5
; Sequence 5, Application US/09963285
; Patent No. US20020090707A1
; GENERAL INFORMATION:
; APPLICANT: Enerbck, Sven
; APPLICANT: Kirook, Katarina
; APPLICANT: Ron Dahl, Lena
; APPLICANT: Wasserman, Wyeth
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-042001
; CURRENT APPLICATION NUMBER: US/09/963,285
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: SE 0004102-0
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/238,897

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; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: SE 0003435-5
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 6021
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1649)...(438)
US-09-963-285-5

Query Match          62.6%; Score 14.4; DB 10; Length 6021;
Best Local Similarity 54.5%; Pred. No. 1.8e+02;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNATNCCNGNTTYMGNTNG 22
    ||:|||||:|:|:|:|:|:|
Db 2862 GGCCTGCCCGCTTCAGCGTGG 2883

RESULT 10
US-09-963-285-1
; Sequence 1, Application US/09963285
; Patent No. US2002090707A1
; GENERAL INFORMATION:
; APPLICANT: Enerbeck, Sven
; APPLICANT: Krook, Katrina
; APPLICANT: Rondahl, Lena
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-042001
; CURRENT APPLICATION NUMBER: US/09/963,285
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: SE 0004102-0
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/238,897
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: SE 0003435-5
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6458
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2235)...(3737)
US-09-963-285-1

Query Match          62.6%; Score 14.4; DB 10; Length 6458;
Best Local Similarity 54.5%; Pred. No. 1.8e+02;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 GGNATNCCNGNTTYMGNTNG 22
    ||:|||||:|:|:|:|:|:|
Db 3030 GGGCTGCCTGGCTTCAGCGTGG 3051

RESULT 11
US-09-974-879-57
; Sequence 57, Application US/09974879
; Publication No. US20030028003A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P2
; CURRENT APPLICATION NUMBER: US/09/974,879
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/239,893
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; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 09/818,683
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 09/305,736
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: PCT/US98/23435
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/064,911
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,912
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,983
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,900
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,988
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,987
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,908
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,984
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,985
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/066,095
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,090
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 611
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (536)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-974-879-57

Query Match          61.7%; Score 14.2; DB 9; Length 536;
Best Local Similarity 56.5%; Pred. No. 1.7e+02;
Matches 13; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 1 GGNATNCCNGNTTYMGNTNG 23
    ||:|||||:|:|:|:|:|
Db 295 GGGTTKCCAGGCTTGAGGCTGG 317

RESULT 12
US-09-938-842A-1726
; Sequence 1726, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
```

;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: US 60/300,111
;; PRIOR FILING DATE: 2001-06-22
;; NUMBER OF SEQ ID NOS: 5379
;; SEQ ID NO 1726
;; LENGTH: 1488
;; TYPE: DNA
;; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1726

Query Match
Best Local Similarity 56.5%; Score 14.2; DB 9; Length 1488;
Matches 13; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGNVTNCCNGGNTTYMGNTNG 23
DB 847 GGTCTCCGCGGCTTTAGAGTTGG 869

RESULT 13
US-09-822-830A-14

;; Sequence 14, Application US/09822830A
;; Patent No. US20020142952A1
;; GENERAL INFORMATION:
;; APPLICANT: Genetics Institute, Inc.
;; APPLICANT: Wong, Gordon G.
;; APPLICANT: Clark, Hilary
;; APPLICANT: Fechtel, Kim
;; APPLICANT: Agostino, Michael J.
;; APPLICANT: Howes, Steven H.
;; APPLICANT: Resnick, Richard J.
;; APPLICANT: Gulukota, Kamalakari
;; APPLICANT: Graham, James R.
;; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
;; FILE REFERENCE: GIN 6402
;; CURRENT APPLICATION NUMBER: US/09/822,830A
;; CURRENT FILING DATE: 2001-03-29
;; PRIOR APPLICATION NUMBER: 60/195,604
;; PRIOR FILING DATE: 2000-04-06
;; NUMBER OF SEQ ID NOS: 631
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 14
;; LENGTH: 2099
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-822-830A-14

Query Match
Best Local Similarity 56.5%; Score 14.2; DB 10; Length 2099;
Matches 13; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGNVTNCCNGGNTTYMGNTNG 23
DB 1639 GGGTTCCAGCCTTGAGAGTGG 1661

RESULT 14
US-09-954-456-542

;; Sequence 542, Application US/09954456
;; Patent No. US20020115057A1
;; GENERAL INFORMATION:
;; APPLICANT: Young, Paul
;; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
;; FILE REFERENCE: 689290-76
;; CURRENT APPLICATION NUMBER: US/09/954,456
;; CURRENT FILING DATE: 2001-09-18
;; PRIOR APPLICATION NUMBER: US/60/233,617
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: US/60/234,052
;; PRIOR FILING DATE: 2000-09-20
;; PRIOR APPLICATION NUMBER: US/60/234,923
;; PRIOR FILING DATE: 2000-09-25

;; PRIOR APPLICATION NUMBER: US/60/235,134
;; PRIOR FILING DATE: 2000-09-25
;; PRIOR APPLICATION NUMBER: US/60/235,637
;; PRIOR FILING DATE: 2000-09-26
;; PRIOR APPLICATION NUMBER: US/60/235,638
;; PRIOR FILING DATE: 2000-09-26
;; PRIOR APPLICATION NUMBER: US/60/235,711
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: US/60/235,720
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: US/60/235,840
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: US/60/235,863
;; PRIOR FILING DATE: 2000-09-27
;; NUMBER OF SEQ ID NOS: 2276
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 542
;; LENGTH: 2242
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-954-456-542

Query Match
Best Local Similarity 56.5%; Score 14.2; DB 10; Length 2242;
Matches 13; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGNVTNCCNGGNTTYMGNTNG 23
DB 1256 GGGTTCCGCGGCTTTAGAGTTGG 1278

RESULT 15
US-09-921-771-5

;; Sequence 5, Application US/09921771
;; Patent No. US20020081284A1
;; GENERAL INFORMATION:
;; APPLICANT: Li, Dean Y.
;; TITLE OF INVENTION: Manipulation of Arterial-Venous Identity
;; FILE REFERENCE: 10402-011
;; CURRENT APPLICATION NUMBER: US/09/921,771
;; CURRENT FILING DATE: 2001-08-03
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 5
;; LENGTH: 2274
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-921-771-5

Query Match
Best Local Similarity 56.5%; Score 14.2; DB 10; Length 2274;
Matches 13; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGNVTNCCNGGNTTYMGNTNG 23
DB 1207 GGGTTCCGCGGCTTTAGAGTTGG 1229

Search completed: March 10, 2003, 06:46:24
Job time : 63.5 secs

